A TOTAL STATE OF THE

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GenCore yersion 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 20, 2002, 10:27:17; Search time 30 Seconds (without alignments) 66.644 Million cell updates/sec Run on:

US-08-854-764-7 96

1 DSEEDEEHTIITDTELPP 18 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

747574 Total inumber of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_032802 Database

/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/Aa1997.DAT./SIDSI/gcgdata/hold-geneseq/geneseqp-embl/Aa1998.DAT./SIDSI/gcgdata/hold-geneseq/geneseqp-embl/Aa1999.DAT./SIDSI/gcgdata/hold-geneseq/geneseqp-embl/Aa3000.DAT./SIDSI/gcgdata/hold-geneseq/geneseqp-embl/Aa2000.DAT./SIDSI/gcgdata/hold-geneseq/geneseqp-embl/Aa2001.DAT./SIDSI/gcgdata/hold-geneseq/geneseqp-embl/Aa2001.DAT. /gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT /geneseqp-embl/AA1989 /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1983. data/hold-geneseq/geneseqp-embl/AA1987. /gcgdata/hold-geneseq/geneseqp-embl/AA1990 qeneseqp-embl/AA199 /geneseqp-embl/AA199 geneseqp-embl/AA198 /SIDSI/gcgdata/hold-geneseq/genesegp-embl/AA198 /SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA198 /gcgdata/hold-geneseg/ gcgdata/hold-geneseg, /gcgdata/hold-geneseg, ′gcgdata∕hold-geneseg, /gcgdata/hold-geneseg /SIDS1/qcq /SIDS1/gcg /SIDS1/gcg /SIDS1/qcd /SIDS1/ /SIDS1/ /SIDS1/ /SIDSI /SIDS1 SIDS /SIDS1 /SIDS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		æ					
Result	,	Query	:	1			
2	Score	Match	Match Length DB ID	8	ΩI	Description	10n
1	96	100.0	18	17	AAR92013	TFPI N-	terminal pe
	96	100.0	160	13	AAR23800	LACI fra	LACI fragment 1 -
m	96	100.0		17	AAW00017	TFPI Ch.	TFPI chimeric prot
4	96	100.0		22	AAU02971	Angiote	nsin conver
S	96	100.0		12	. AAR11169	Ser (Asp	1-Thr255)-E
9	96	100.0		12	AAR11171	Ser-(As)	p1-Glu245)-
7	96	100.0		12	AAR11172	Ser-(As)	p1-Ser248)-
<b>σ</b>	96	100.0		12	AAR11170	Ser-(As	ser-(Asp1-Ile253)-
9	96	100.0		17	AAR92265	TFPI mu	FFPI mutein, Lys36
10	96	100.0	276	17	AAR92012	TFPI mu	FFPI mutein K36R.
11	96	100.0		18	AAW30311	Recombi	Recombinant non-gl

Human tissue facto Non-qlycosylated T	Human tissue facto	Lipoprotein-associ	Human lipoprotein-	Tissue factor path	Human lipoprotein	Obiquitin-TFPI fus	Human mutant tissu	Human tissue facto	(Asp1-Thr161)-EPI	LAC1 gene product.	LACI N-terminal (G	Novel human protei	white s	Tissue factor inhi	Tissue factor inac	Tissue factor inhi	RRP3 telomerase-as	-	-		Arabidopsis thalla	Porcine adenovirus	Arabidopsis thalia	tn enco	human	human	Novel human diagno	Rat IP3 receptor.	Chlamydia pneumoni	Human protein sequ	Human Fchd531 gene	Protein encoded by
AAW61535 AAR37312	AAP92002	AAR81884	AAR78389	AAR67994	AAY49557	AAR92011	AAY70272	AAY70:273	AAR11167	AAR42309	AAR55840	AAW36796	AAG85011	AAR37859	AAR63232	AAR75880	AAR95607	AAW26623	AAG45731	AAG17608	AAG45730	AAY95939	AAG45700	AAU15066	ABG01620	ABG03191	ABG14001	AAR88125	AAY 34969	AAM25908	AAW36002	AAY45013
19	10	16	16	16	20	11	21	21	12	14	15	18	22	14	15	16	11	18	21	21	21	21	21	22	22	22	22	11	20	22	18	71
276	304	304	304	304	304	352	304	304	189	304	23	224	1036	22	22	22	1085	1189	111	118	125	198	467	759	831	831	1492	2670	406	423	570	570
100.0	100.0	100.0	100.0	100.0	100.0	100.0	6.96	6.96	93.8	93.8	9.68	52.6	51.0	50.0	50.0	50.0	50.0	49.0	47.9		47.9		47.9	47.9	47.9	47.9	47.9	47.9	46.9	46.9	46.9	46.9
96	96	96	96	96	96	96	93	93	90	90	98	50.5	49	48	48	48	48	47	46	46	46	46	46	46	46	46	46	46	4.5	45	45	45
12	14	15	16	17	18	19	20	21	22	23	24	25	. 56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

## ALIGNMENTS

AAR92013 standard; Peptide; 18 AAR92013 RESULT

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AAR92013;

(first entry)

08-MAY-1996

TFPI N-terminal peptide.

Factor-Xa; binding protein; tissue factor inhibitor; factor pathway inhibitor; TFPI; TFPI-2; Factor-VIIa; factor; Tissue tissue

lipoprotein associated coagulation inhibitor;
extrinsic pathway inhibitor; sepsis; septic shock; Saccharomyces cerevisiae

Synthetic.

W09604377-A1

15-FEB-1996.

95WO-US09377. 25-JUL-1995; 94US-0286530. (CHIR ) CHIRON CORP. 05-AUG-1994;

Creasey AA, Innis MA;

WPI; 1996-129393/13.

Production of tissue factor pathway inhibitor in yeast cells - with isolation from the insoluble cell fraction, used to treat or prevent

sepsis

or septic

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0

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RESULT
AAR23800
 Query Match
Best Local S
Matches 18
                            The sequence given is a peptide fragment of lipoprotein associated coaglutination inhibitor (LACI) having the sequence of residues 1 to 160 of the 276 residue mature LACI protein. This peptide fragment corresponds to Kunitz domains of LACI and can be used for inhibiting Factor VIIa/tissue factor enzymatic complex formation. Factor VIIa is the activated form of factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The N-terminal peptide (AAR92013) of recombinant tissue factor pathway inhibitor (TFPI) produced in Saccharomyces cerevisiae cells transformed with vector plasmid pLACI 4.1 corresponded to authenic mature TFPI. This showed that expression of a
                                                                                                                                                                          Peptide fragments of lipoprotein-associated coagulation inhibitor - used for inhibiting Factor Xa prodn. or inhibiting Factor VIIA tissue factor complex formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5106833-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR23800 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        provided biologically active TFPI having the correct N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to authenic mature TFPI. This showed that expression of a ubiquitin/TFPI protein fusion in yeast, with subsequent removal of the ubiquitin fusion partner within the yeast cells.
Sequence
                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                          WPI; 1992-159405/19
                                                                                                                                                                                                                                                                          Broze GJ,
                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                       23-JUL-1987;
23-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein-associated coaglutination inhibitor; kuintz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LACI fragment 1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dseedeehtiitdtelpp 18
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I Similarity 100.0%;
18; Conservative
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                                                                                                                                                                                                                                                                        Girard TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 16; 36pp;
                                                                                                                                            Fig 1; 9pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                      87US-0077366.
87US-0123753.
89US-0301779.
                                                                                                                                                                                                                                                                                                                                                                                                      89US-0301779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 160 AA
                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor
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Query Match Best Local Similarity

100.0%;

Score Pred.

96;

DB 13; 4.5e-07;

Length 160;

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RESULT
AAW00017
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                                                                                                             Kunitz-type domains are covered within the scope of the invention. Chimeric proteins comprising the kunitz-type domains from TPDL or TPPL-2, may also comprise an alternative glycosaminoglycan Sinding peptide selected from those given in AA892266-73. The chimeric proteins and muteins may be used in a pharmaceutical composition for the
                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a chimeric protein containing the thist and second kunitz-type domain derived from tissue factor pathway inhibitor (TFPI). This sequence has a Lys to Arg mutation in the Pi-reactive domain of the first kunitz-type domain, and an Asn to Gln mutation in the Pi-reactive domain of the second Kunitz-domain. The Kunitz-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunitz-type domain; C-terminal tail; tissue factor pathway inhibitor; TFPI; TFPI-2; cell|surface localisation; glycosaminoglycan; heparin; phospholipid; binding; chimeric protein; mutein; substitution; phospholipid; binding; chimeric protein; mutein; substitution;
treatment of sepsis, septic shock and thrombosis disorders. The may be generally useful in the treatment of diseases caused by up-regulation of tissue factor bought on by injury, trauma, entire, cancer, IL-1 or other agents or conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 19; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric protein comprising Kunitz-type domains from TPPI-1 and -2 - used for the treatment of septic shock and thrombosis disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW00017;
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                                                                                                                                                                                                                                                               localisation by glycosaminoglycan (including heparin) or phospholipid binding. Chimeric proteins such as this, having one or more substitutions exclusively in the Pl-reactive site of one or more
                                                                                                                                                                                                                                                                                                                                                    domains are highly basic sequences and may be involved in cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-129394/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Creasey AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFPI chimeric
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s factor; interleukin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0286521
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36 .
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117
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97..147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Asn117Glr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "First Kunitz-type domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Second Kunitz-type domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
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                                 endotoxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                            The proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor
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225 AA;

8 g

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as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis.
                                                              Sequence
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                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor ic, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothalial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; multiple sclarosis; immune disorder; sarcoidosis; multiple sclarosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents an angiotensin converting enzyme splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis,
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                      Angiotensin converting enzyme (ACEV) splice variant protein #71
                                                                                                                      ;
0
                                                                              Length 161;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bernstein J;
                                                                          Score 96; DB 17;
Pred. No. 4.6e-07;
                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khosravi R,
                                                                                                                                                                                                                                                                                                  AAU02971 standard; Protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 71; 519pp; English.
                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vascular disorder; asbestosis.
                                                                            100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000; 2000WO-IL00766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 991L-0132978.
991L-0133455.
                                                                                                                                                           1 DSEEDEEHTIITDTELPP 18
                                                                                                                                                                                (first entry)
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levine Z, David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-336004/35.
                                                                                                 Best Local Similarity
Matches 18; Conserv
                    161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS06071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001.
                Sequence
                                                                                                                                                                                                                                                                                                                                       AAU02971;
                                                                              Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the region from Arg246 to Lys275. This analogue is an example of such a peptide; it corresponds to anino acids I to 255 of pective EPI with an additional N-terminal Ser residue. The analogue gain be used in a therapeutic composition to treat patients having coagulation disorders or cancer. The analogue has a longer half-life than
                                                                                                                                                                                                                                                                                                                                                                                                                            Extrinsic pathway inhibitor protein; tissue plasminogen activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preferred EPI analogues of the invention comprise the first two kunitz domains of native EPI and have one or more amino acids deleted in the region Glu148 to the C-terminal Met276, especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 256;"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 0;
      Length 225;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extrinsic pathway inhibitor protein analogue - useful as anticoagulant and anti-cancer agent due to low or no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 96; DB 12;
100.0%; Pred. No. 7.6e-07;
tive 0; Mismatches 0;
                                                    ö
      Score 96; DB 22;
Pred. No. 6.6e-07;
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also AAQ10992-4 and AAR11170-R11172.
                                                                                                                                                                                                                                                 AAR11169 standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 20; 39pp; English.
                                                  0
                                                                                                                                                                                                                                                                                                                                                                                 Ser(Aspl-Thr255)-EPI analogue.
      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90WO-DK00212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89DK-0004080
                                                                                             1 DSEEDEEHTIITDTELPP 18
                                                                                                                 29 dseedeehtiitdtelpp 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                   kunitz domain; coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DSEEDEEHTIITDTELPP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 dseedeehtiitdtelpp. 19
                                                                                                                                                                                                                                                                                                                                   21-MAY-1991 (first entry)
Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nordfang O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heparin-binding capacity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-087248/12.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rasmussen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                          AAR11169;
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cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such

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RESULT
AAR11171
ID AAR1
XX AAR1
XX AAR1
XX 21-1
DT 21-1
DX Ser
XX Ext
KW kun
XX XX
OS Syn
XX YN
PN WO9
XX
RESULT
AARI1172
ID AARI
XX AARI
AC AARI
XX AARI
XX Ser-
XX Ser-
XX Exti
XW Exti
XW kund
XX Synt
XX Synt
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           Preferred EPI analogues of the invention comprise the first two kunitz domains of native EPI and have one or more amino acids deleted in the region Glu148 to the C-terminal Met276, especially in the region from Arg246 to Lys275. This analogue is an example of such a peptide; it has amino acids 246 to 261 of native EPI deleted with an optional N-terminal Ser residue. The analogue can be used in a therapeutic composition to treat patients having coagulation disorders or cancer. The analogue has a longer half-life than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Extrinsic pathway inhibitor protein analogue - useful as anticoagulant and anti-cancer agent due to low or no heparin-binding capacity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ser-(Aspl-Glu245)-(Glu262-Met276)-EPI analogue
            Synthetic.
                                                                             Ser-(Aspl-Ser248)-(Val264-Met276)-EPI analogue.
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 20; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extrinsic pathway inhibitor protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR11171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR11171 standard; Protein;
                                       kun1tz
                                                  Extrinsic pathway inhibitor protein; tissue plasminogen activator
                                                                                                       21-MAY-1991
                                                                                                                                                          AAR11172 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                 See also AAQ10992-4 and AAR11169-R11170, AAR11172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-087248/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OVO ( OVON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kunitz
                                                                                                                                 AAR11172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                        DSEEDEEHTIITDTELPP 18
                                                                                                                                                                                                                         dseedeehtiitdtelpp 19
                                                                                                                                                                                                                                                                                                                                            261 AA;
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NORDISK A/S
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nordfang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89DK-0004080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90WO-DK00212
                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
                                                                                                                                                          262 AA
                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                       Score 96; DB 12;
Pred. No. 7.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ξ
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue plasminogen
                                                                                                                                                                                                                                                                                                   Length 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kunitz domains of native EPI and have one or more amino acids deleted in the region Glu148 to the C-terminal Met276, especially in the region from Arg246 to Lys275. This and a pexample of such a peptide; it has amino acids 249 to 263 of native EPI deleted with an optional N-terminal Ser residue. The analogue can be used in a therapeutic composition to treat patients having coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extrinsic pathway inhibitor protein analogue anticoagulant and anti-cancer agent due to lo heparin-binding capacity
                                                                                                                           07-MAR-1991.
                                                                                                                                                                                                                       Ser-(Asp1-Ile253)-(Ile266-Met276)-EPI analogue
                                                                                                                                                                                                                                                                                     AAR11170 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 20; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rasmussen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1991
                     WPI; 1991-087248/12
                                                                                  18-AUG-1989;
                                                                                                                                                W09102753-A.
                                                                                                                                                                   Synthetic.
                                                                                                                                                                                         kunitz
                                                                                                                                                                                                  Extrinsic pathway inhibitor
                                                                                                                                                                                                                                                                 AAR11170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preferred EPI analogues of the invention comprise the first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9102753-A
                                         Rasmussen
                                                                                                                                                                                                                                             21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders or cancer.
full-length EPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVO ) NOVO
                                                            OAON ( OAON)
                                                                                                      17-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAQ10992-4
                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                              1 DSEEDEEHTIITDTELPP 18
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                                                                                                                                                                                                                                                                                                                                         dseedeehtiitdtelpp 19
                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%;
1 Similarity 100.0%;
18; Conservative (
                                                                                                                                                                                         domain;
                                        J, - Nordfang
                                                                                                                                                                                                                                                                                                                                                                                                                                        262
                                                             NORDISK A/S
                                                                                                                                                                                                                                           (first entry)
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                                                                                  89DK-000408C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89DK-0004080
                                                                                                      90WO-DK00212
                                                                                                                                                                                         coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90WO-DK00212
                                                                                                                                                                                                                                                                                                                                                                                                                                                            and AAR11169-R11171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The analogue has a longer half-life than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                      265 AA
                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                 Score 96; DB 12;
Pred. No. 7.8e-07;
Mismatches 0;
                                                                                                                                                                                                  tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ie - useful as
low or no
                                                                                                                                                                                                                                                                                                                                                                                                      Length 262;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Extrinsic pathway inhibitor protein analogue -

useful as

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                                                                                                                                                                                                            Gaps
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                                                         kunitz domains of native EPI and have one or more amino acids.
deleted in the region Gluid8 to the Cterminal Metz76, sepecially
in the region from Arg246 to Lys275. This analogue is an example of
such a peptide; it has amino acids 254 to 265 of native EPI deleted
with an optional N-terminal Ser residue. The analogue can be used
in a therapeutic composition to treat patients having coagulation
disorders or cancer. The analogue has a longer half-life than
                                                analogues of the invention comprise the first two
                                                                                                                                                                                                            ö
                                                                                                                                                                                        Score 96; DB 12; Length 265; Pred. No. 7.9e-07;
                                                                                                                                                                                                            Indels
   2
   or
                                                                                                                                      See also AAQ10992-4 and AAR11169, AAR11171-R11172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Second Kunitz-type domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Third Kunitz-type domain"
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "First Kunitz-type domain"
anticoagulant and anti-cancer agent due to low heparin-binding capacity
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240..276 /note= "C-terminal tail"
                                                                                                                                                                                                                                                                                                 AAR92265 standard; peptide; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- Lys36Arg
                           Claim 5; Page 20; 39pp; English.
                                                                                                                                                                                                           ö
                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0286521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US09464
                                                                                                                                                                                                                              DSEEDEEHTIITOTELPP 18
                                                                                                                                                                                                                                       2 dseedeehtiitdtelpp 19
                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                           TFPI mutein, Lys36Arg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-129394/13.
                                                                                                                                                           265 AA;
                                                                                                                             full-length EPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                EPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9604378-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                        30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Creasey AA,
                                                Preferred
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                    AAR92265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
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ID AAR9
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This sequence represents a mutein of tissue factor pathway inhibitor (TFPI). This sequence has a Lys to Arg mutation in the Pi-reactive domain of the first Kunitz-type domain. The Kunitz-type domains are highly basic sequences and may be involved in cell surface localisation by glycosaminoglycan (including heparin) or phospholipid binding. Muteins such as this, having one or more substitutions exclusively in the Pi-reactive site of one or more Kunitz-type domains are covered by the scope of the invention. Chimeric proteins comprising the kunitz-type domains from TFPI or TFPI-2, may also comprise an alternative glycosaminoglycan binding peptide selected from those given in AR92266-73. The chimeric proteins and muteins may be used in a pharmaceutical composition for the treatment of sepsis, septic shock cand thrombosis disorders. The proteins may be generally useful in the treatment of diseases caused by the up-regulation of tissue factor bought on by injury, trauma, endotoxin, TNF, cancer, IL-1 or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Production of tissue factor pathway inhibitor in yeast calls - with isolation from the insoluble cell fraction, used to treat or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue factor pathway inhibitor; TFPI; TFPI-2; Factor-VIIa; tissue factor; Factor-Xa; binding protein; tissue factor inhibitor; lipoprotein associated coagulation inhibitor; extrinsic pathway inhibitor; sepsis; septic shock;
himeric protein comprising Kunitz-type domains from TFPI-1 and '-2 used for the treatment of septic shock and thrombosis disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ý.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 96; DB 17;
Pred. No. 8.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
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                                                                       Disclosure; Page 8; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR92012 standard; Protein; 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DSEEDEEHTIITDTELPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sepsis or septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Innis MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-129393/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFPI mutein K36R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9604377-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Creasey 'AA'
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English.

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RESULT 11
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Best Local
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                Ag. formulation of tissue factor pathway inhibitor - contains charged polymer, e.g. dextran sulphate, to facilitate solubilisation, formulation purification and refolding of protein
                                                                                                            WPI; 1997-087056/08.
                                                                                                                                                                                                                                                                                                            07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue factor pathway inhibitor; TFPI; human; tissue factor inhibitor; Lipoprotein-associated coagulation inhibitor; coagulation inhibitor; TFI; LACI; extrinsic pathway inhibitor; protein refolding; clot-inhibitor; protein solubility modification; EPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                        Pattison
                                                                                                                                                                                                                                            (CHIR ) CHIRON (SEAR ) SEARLE
                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant non-glycosylated TFPI.
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                                                                                                                                                                             Hallenbeck RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide
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                                                                                                                                                                 Bild GS, c..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                      GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Factor-VIIa/TF/Xa binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                      Rana RK,
                                                                                                                                                                                                                                            CORP.
                                                                                                                                                                                                                                                                                                            95US-0477677.
95US-0473668.
                                                                                                                                                                                                                                                                                                                                                                             08660Sn-0M96
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122..143
189..239
198..222
214..235
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97..147
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35..59
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                                                                                                                                                                                         Chen B,
                                                                                                                                   IMS, Tsang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "phosphorylated to varying degrees,
affect TFPI function"
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                                                                                                                                                                        B, Dorin GJ,
Johnson GV,
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Pred. No.
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                                                                                                                                                                           Gustafson
Johnson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 17;
8.3e-07;
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                                                                                                                                                                           Madani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                            Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified or refolded using the methods of the invention. One modified or refolded using the methods of the yadding an aqueous solution of a CP to reduce inter and intra-molecular interactions between the charged domains of the protein. The second method is for refolding an improperly folded or denatured protein (e.g. TFPI), and comprises adding CP to a solution of the protein prior to allowing the protein to refold. The methods are particularly useful for solubilising, formulating, purifying and refolding proteins (especially TFPI) which have been engineered by genetic recombination and produced in bacterial, yeast or expectation of the protein protein to a formulating the protein protein to allowing the protein to refold.
Disulfide-bond Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the optimum codons for expression in E. coli, to allow for expression of this protein in the bacteria. TFPI is used in the aqueous formulation of the invention. The aqueous formulation also includes a charged polymer (CP), preferably a sulphated polysaccharide (such as heparin or dextran sulphate) or a polyphosphate, preferably immobilised on a solid support. The CP is added to aid the correct refolding of TFPI. TFPI can also be modified or refolded using the methods of the invention. One method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein. TFPI is also known as Lipoprotein-associanhibitor (LACI), extrinsic pathway inhibitor (Finhibitor (TFI). The DNA encoding this sequence
                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                  angiogenesis-related diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                              Human tissue
                                            Domain
                                                                          Modified-site
                                                                                          Disulfide-bond
                                                                                                                       Modified-site
                                                                                                                                      Disulfide-bond
                                                                                                                                                                                 Doma in
                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                       key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                Human tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW61535 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other cells in a form that has a non-native tertiary structure. coagulation inhibitor which has clot-inhibiting properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 86pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents the human tissue factor pathway inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 100.0%; similarity 100.0%; 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
                                                                                                                                                                                                                                                                                                                                                                                factor pathway inhibitor;
-related disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                            factor pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is also known as Lipoprotein-associated coagulati
I), extrinsic pathway inhibitor (EPI) and Tissue
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                                                                                       /note= "P
122..143
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97..147
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97..147
/note-
189..23
198..22
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26..76
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                          167
                                              189.
                                                         /note- "N-glycosylated"
                                                                                                                                                                                                                                                                          /note-
 ..239
                                            ..239
                          "Kunitz-3 type protease
                                                                                                       "N-glycosylated
                                                                                                                                                                 "Kunitz-2
                                                                                                                                                                                                                                          "Kunitz-1 type protease inhibitor
                                                                                                                                                                                                                                                                         "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor (TFPI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96; DB Pred. No. 8.3); Mismatches
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                                                                                                                                                                type protease inhibitor domain*
                                                                                                                                                                                                                                                                                                                                                                                 arthritis;
                                                                                                                                                                                                                                                                                                                                                                              TFPI; TFPI-2; cell proliferation;
arthritis; macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
                            inhibitor domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was altered to contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 276;
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                                                                                    4.0
                                                                                                                                                                                                                                         domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the human tissue factor pathwitch (TPPI). The invention provides compositions using and its homologs, e.g.TPPI-2 (AAW61536), for inhibiting cell proliferation. The compositions are claimed to be useful for an angiogenesis related disease, such as cancer, arthritis, m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Pages 23-24; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases e. retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition comprising tissue factor pathway inhibitor for inhibiting cell proliferation - for treating angiogenesis related diseases e.g. cancer, arthritis, macular degeneration and diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green.
        US5212091-A
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-446947/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ENTR-) ENTREMED INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-FEB-1998;
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                            Disulfide-bond Disulfide-bond
                                               Disulfide-bond
                                                                     Disulfide-bond
Disulfide-bond
                                                                                       Disulfide-bond
                                                                                                                                                            Non-glycosylated; tissue factor pathway inhibitor; TFPI; multivalent; lipoprotein associated coagulation inhibitor; inhibitor; Kunitz-type; coagulation; domain; factor VIIa; LACI; tissue factor; factor Xa;
                                                                                                                                                                                                                                                                                                                                                                                                                              degeneration or diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9834634-A1
                                                                                                                                Escherichia
                                                                                                                                                                                                                                               AAR37312;
                                                                                                                                                                                                                                                                 AAR37312 standard;
                                                                                                                                                    complex;
                                                                                                                                                                                                     Non-glycosylated TFPI
                                                                                                                                                                                                                           20-SEP-1993
                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                    coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papathanassiu AE;
                                                                                                                                                                                                                                                                                                                                                                                                            276 AA;
                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative (
                                                                                                                                coli
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..98₩0-US02699.
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                           106..130
122..143
189..239
198..222
214..235
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228
                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-glycosylated"
                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                  277
                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                    Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                   8.3e-07
                                                                                                                                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                        e useful for inhibiting arthritis, macular
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                              276;
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a non-glycosylated form of tissue factor pathway inhibitor (TFFI). TFFI is alternatively known as lipoprotein associated cosgulation inhibitor (LACI). TFFI is a multivalent Kunitz-type inhibitor of coagulation. The primary amino acid sequence of TFFI shows that it contains a highly negatively charged amino terminus, three tandem kunitz-type inhibitory domains and a highly positively charged carboxyl terminal. The first kunitz domain of TFFI is needed for the inhibition of factor VIIa/tissue factor complex and the second kunitz domain of TFFI is responsible for the inhibition of factor VIIa/tissue factor to shibition of factor Xa. The function of the third kunitz domain is unknown. TFFI is thought to act in vivo to limit the initiation of factor YIIa/tissue factor the inhibition of factor YIIa/tissue factor Y
                                                                               Protein
Region
                                                                                                                                                                                                                                         Кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor in high yield - comprises culturing E.coli cells transformed with replication expression vector and subjecting isolated inclusion bodies to sulphitolysis or redn. with
                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is unknown. TFPI is thought to act in vive to action Xa:TFPI:factor of coagulation by forming an inert, quaternary factor Xa:TFPI:factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1992;
                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                     protease
                                                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                              tissue factor
ase inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of non-glycosylated form of tissue factor pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 factor inhibitor (TFI)..
                                                                                                                                                                                                                                                                                                                                                     factor inhibitor;
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                                                                                                                                                     /note=
28..29
                                                                                                      /note= "Possible site for signal peptidase" 29..304
                                                                                                                                                                          /label= Signal_region
/note= "A-T rich"
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gustafson ME,
                                                                                                                                                                                                                                                                                                                                r inhibitor; TFT; human placenta lambda-P9 clone; gene superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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Pred. No. 8.3
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hes 0;
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Region Region

145.

195..197

"Potential

N-linked

note-

"Potential N-linked

glycosylation site" glycosylation site"

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Amino acid sequence of tissue factor inhibitor (TFI) cDNA isolate from inabda-P9 clone of human placenta cDNA library. Domains discerned include: highly negatively charged N-terminal: highly positively charged carboxy-terminal; intervening portion consisting of 3 homologous domains with sequences typical of Kunitz-type enzyme inhibitors. Based on homology study, it appears to be a member of the basic protease inhibitor gene superfamily. Sequences in misc. regions in feature table above have been independently confirmed by amino acid sequence analysis.
/note= "Potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human tissue factor inhibitor
- used in study of coagulation cascade for agents
which inhibit factor Xa and Factor VIIA-TF
                         //note= "See comments below"
/note= "See comments below"
                                                                                               /note= "See comments below"
                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                 Kretzmer KK, Wun TC;
                                                                                                                                                                                                                              87US-0123753.
                                                                                                                                                                                               88EP-0870127
                                                                                                                                                                                                                                                              (MONS ) MONSANTO CO (UNIW).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Figure 3; 14pp;
                                                                                                                                                                                                                                                                                                                            WPI; 1989-159483/22.
N-PSDB; AAN90108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 AA
                                                                                                                                                                                               22-JUL-1988;
                                                                                                                                                                                                                           23-NOV-1987;
                                                                                                                                                        31-MAY-1989.
                                                      1.6"
                                                                                                                                EP318451-A.
                                                                                                                                                                                                                                                                                                 Broze GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                               Region
                 Region
                                                                                Region
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Gaps ö 100.0%; Score 96; DB 10; Length 304; 100.0%; Pred. No. 9.2e-07; Ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 18; Conservative Query Match

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1 DSEEDEEHTIITOTELPP 18

셤 ö

AAR81884 standard; protein; 304 AA (first entry) 18-MAR-1996 AAR81884; Ä 

Lipoprotein-associated coagulation inhibitor (LACI).

Lipoprotein-associated coagulation inhibitor; LACI; kallikrein; inhibitor; KIP; Kunitz domain; hereditary angloedema.

Homo sapiens

"Kunitz domain LACI-K1" /label- sig\_peptide 50..107 Key Peptide Domain Domain

Location/Qualiflers

/note= "Kunitz domain LACI-K1" 121..178 /note= "Kunitz domain LACI-K2" 213..270

Domain

WO9521601-A2 17-AUG-1995. 

/note= "Kunitz domain LACI-K3"

95WO-US00299 LO-MAR-1994; 11-JAN-1995;

94US-0208264. 11-JAN-1994;

(PROT-) PROTEIN ENG CORP.

Ladner RC, Markland

WPI; 1995-292934/38.

domain homologous Kallikrein inhibiting proteins comprising a Kunitz domain homologe to bovine pancreatic trypsin inhibitor - useful for preventing or treating disorders attributable to excessive kallikrein activity, eg. in hereditary angloedema

Disclosure; Page 24; 46pp; English.

AAR81884 is the human lipoprotein-associated coagulation inhibitor LACI. The Kunitz domain, LACI: Ki, of LACI is a Kallikrein inhibiting protein (KIP) upon which the claimed KIPs of the invention are based. The KIPs can be used for treating or preventing disorders attributable to excessive kallikrein activity, e.g. hereditary angloedema. The KIPs can also be used for assaying, purifying and in vivo inaging of kallikrein.

304 AA Sequence

Gaps ö Length 304; Indels Score 96; DB 16; Pred. No. 9.2e-07; Mismatches ö 100.0%; 100.0%; Query Match Best Local Similarity 100. Matches 18; Conservative

1 DSEEDEEHTIITDTELPP 18 qq ò

Search completed: September 20, 2002, 10:28:38 Job time: 81 sec

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GenCore version 4.5 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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 DВ
                                                               PCT-US95-09464-9
US-07-844-297-1
US-08-026-145-2
US-08-446-646-9
US-08-676-125A-18
                                                                                                                        US-08-286-521-9

US-08-436-175-9

US-08-796-850-1

US-08-854-764-3

US-08-943-682-9

PCT-US95-09377-3
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US-07-828-920A-
US-08-437-841-9
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-828-920A-1
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18, Appl
1, Appli
25, Appl
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1, Appl
9, Appl
9, Appl
9, Appl
9, Appl
1, Appl
1, Appl
3, Appl
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.

ALIGNMENTS  -7 Application US/08854764 6103500	100.0 304 4 US-09-421-097-25 Sequence 100.0 354 5465/83-2 Sequence 100.0 352 3 US-08-854-764-2 Sequence 100.0 352 3 US-08-854-764-2 Sequence 200.0 352 5 PCT-US95-09377-2 Sequence 200.0 352 5 PCT-US95-09377-2 Patent No. 52.6 224 3 US-08-630-916A-50 Sequence 200.0 1085 2 US-08-630-916A-50 Sequence 200.0 1085 2 US-08-938-534-28 Sequence 200.0 1085 2 US-09-195-868-15 Sequence 200.0 1085 2 US-08-826-246-2 Sequence 200.0 1085 2 US-08-944-25-2 Sequence 200.0 1085 2 US-08-925-588-2 Se
	Sequence 25, Appliatent No. 5466783 Sequence 2, Appliatent No. 5466783 Sequence 20, Appliatent No. 5467926 Sequence 50, Appliatent No. 5427926 Sequence 28, Appliaequence 28, Appliaequence 15, Appliaequence 28, Appliaequence 28, Appliaequence 27, Appliaequence 28, Appliaequence 29,

	US-08-854-764-7	a
MOLECULE TYPE: peptide	MOLECUI	٠.
TOPOLOGY: linear	TOPOI	٠.
STRANDEDNESS: single	STRAN	٠.
TYPE: amino acid	TYPE:	٠.
LENGTH: 18 amino acids	LENGI	٠.
SEQUENCE CHARACTERISTICS:	SEQUENC	٠.
INFORMATION FOR SEQ ID NO: 7:	INFORMATI	٠.
LEFAX: 510-655-3542	TELER	٠.
TELEPHONE: 510-601-2585	TELEF	٠.
TELECOMMUNICATION INFORMATION:	TELECON	٠.
REFERENCE/DOCKET NUMBER: 0991.001	REFER	
REGISTRATION NUMBER: 36,914	REGIS	٠.
NAME: Savereide, Paul B.	NAME	٠.
ATTORNEY/AGENT INFORMATION:	ATTORNE	٠.
FILING DATE: 05-AUG-1994	FILIN	٠.
ă	APPLI	٠.
PRIOR APPLICATION DATA:	PRIOR !	٠.
CLASSIFICATION: 435	CLASS	٠.
	FILI	٠.
APPLICATION NUMBER: US/08/854,764	APPLI	٠.
CURRENT APPLICATION DATA:	CURRENT	٠.
SOFTWARE: PatentIn Release #1.0, Version #1.30B	SOFT	٠.
OPERATING SYSTEM: PC-DOS/MS-DOS	OPER!	٠.
COMPUTER: IBM PC compatible	COMPL	٠.
MEDIUM TYPE: Floppy disk	MEDIU	٠.
COMPUTER READABLE FORM:	COMPUTE	٠.
ZIP: 94608	ZIP:	٠.
COUNTRY: USA	COUNT	٠.
	STATE:	٠.
IJ	CITY:	٠.
STREET: 4560 Horton St.	STREE	٠.

Query Match Best Local Similarity

Matches

18;

Conservative

100.0%; Score 96; DB 3; 100.0%; Pred. No. 2.1e-08; tive 0; Mismatches 0;

Length 18,

Indels

0;

Gaps

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                                                SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/437,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96; DB 1;
Pred. No. 2.3e-07;
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APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
ATORNEY/AGENT INFORMATION:
NAME: Saveraide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECHONE: 510-655-3542
TELEFERX: 510-655-3542
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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Patent No. 5589359
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REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 09
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 18; Conservative
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Emeryville
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INFORMATION FOR SEQ ID NO:
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; MOLECULE TYPE:
US-08-437-841-19
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                                                                                                                                                        FILING DATE
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TITLE OF INVENTION: Production of Tissue Factor Pathway
TITLE OF INVENTION: Inhibitor
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CURRENT APPLICATION NO DATA:
APPLICATION NUMBER: PCT/US95/09377
FILING DATE: 25-JULY-1995
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APPLICANT: Inn1s, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
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REGISTRATION NUMBER: 36,914
REFERENCE, POCKET NUMBER: 0991.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                   Sequence 7, Application PC/TUS9509377
GENERAL INFORMATION:
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ADDRESGRE: Chiron Corporation
STREET! 4560 Horton St.
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
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MEDIUM TYPE: Floppy disk
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                             DSEEDERUTIITOTELPP 18
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 18; Conserva
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PCT-US95-09377-7
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APPLICANT:

Innis, Michael

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US-08-943-682-19; Sequence 19, Application US/08943682; Patent No. 6174721
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Best Local Similarity
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Best Local Similarity
GENERAL
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REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
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ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION:
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amino acid
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Pred. No. 2.3e-07;
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Pred. No. 2.3e-07;
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Best Local Similarity
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TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
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FILING DATE: 09-MAY-1995
APPLICATION NUMBER: US 09/
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
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MEDITM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 161 amino acid
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CURRENT APPLICATION DATA:
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                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                    TITLE OF INVENTION: Chimeric Proteins
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MBER: PCT/US95/09464
25-JULY-1995
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Pred. No. 2.3e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 161;
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Gaps

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Length 189;

Score 96; DB 1; Pred. No. 2.7e-07;

100.0%; 100.0%;

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1 DSEEDEEHTIITDTELPP 18
                                                                                                                       29 DSEEDEEHTIITDTELPP 46
Query Match — 100.0
Best Local Similarity 100.0
Matches 18; Conservative
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STREET: 405 Lexington Avenue, Suite 6200
                                                                                                                                                                                                                                                                                                                                                                       Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rasmussen, Jesper
APPLICANT: No. 5312736dfang, Ole Juul
TITLE OF INVENTION: Anticoagulant Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19920127
CLASSIFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 4080/89
FILING DATE: 18-ANG-1989
FILING DATE: 17)ANG)1990
ATONEY/AGENT INFORMATION:
NAME: Zelson, Steve T:
REGISTRATION NUMBER: 30335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 3287.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
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FILING DATE: 19920127
             ATTORNEY/AGENT INFORMATION:
NAME: SAygrated, Paul B.
REGISTRATION NUMBER: 36,914
REPERENCE/DOCKET NUMBER: 0990.100
TELEPHONE: 510-601-2585
TELEPHONE: 510-655-3545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/07828920A
Patent No. 5312736
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative 0
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                                                                                                                                                                                                      161 amino acids
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AMINO ACID
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                                                                                                                                                                                                                                                                                    PE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                   TOPOLOGY: 11near
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PCT-US95-09464-19
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E: No. 53127360 No. 5312736d1sk of No. 5312736th America, Inc. 405 Lexington Avenue, Sulte 6200
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                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920127
CLASSIFICATION: 530
                                          GENERAL INFORMATION:
APPLICANT: Rasmussen, Jesper
APPLICANT: No. 5312736dfang, Ole Juul
TITLE OF INVENTION: Anticoagulant Protein
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 4080/89
FILING DATE: 18-AUG-1989
APPLICATION NUMBER: WO PCT/DK90/00212
FILING DATE: 17)AUG)1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
Sequence 1, Application US/07828920A
Patent No. 5312736
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US-08-437-841-9
; Sequence 9, Application US/08437841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Zelson, Steve T.
REGISTRATION NUMBER: 30335
REFERENCE/DOCKET NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: 212 867 0123
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LENGTH: 276 amino acids
TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.

Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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; MOLECULE TYPE:
US-08-437 841-9
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Best Local Similarity
Matches | 18; Conserv
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                                                                                                                                                                                                                                                                                            equence 9,
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    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                               tent No.
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APPLICANT: Sylnnis, Michael
APPLICANT/ Creasey, Abla
Title Of INVENTION: Chime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 510-601-2585
CURRENT APPLICATION DATA
                                                                                                                                                                             APPLICANT: Creasey, Abla
FITLE OF INVENTION: Chimeric Proteins
UMBER OF SEQUENCES: 37
URRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER
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                                                                                                                                                                                                                                 PPLICANT:
                                                                                                                  STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      COUNTRY:
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TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                              , Application US/08286521 5589359
                                                                                          94608
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                                                                                                                                                  4560 Horton St.
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                                                                                                        USA
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                                                                                                                                                                                                                                                 Innis, Michael
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                                                                                                                                                                     Chiron Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application Patent No. 5696088
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Best Local
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                                                                 INFORMATION FOR SEQ ID NO:
                                             SEQUENCE CHARACTERISTICS
                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polonia
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TOPOLOGY: lin
                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 09-MAN CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 05-AUC
TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Emeryville
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                                                                                             TELEPHONE:
                                                                                                                              REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                         APPLICATION NUMBER: US 08/286,521 FILING DATE: 05-AUG-1994
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                                                                                                                                                             Savereide, Paul
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                                276 amino acids
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single
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Pred. No.
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Length 276;
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/note= "Potential site for N-linked glycosylation"
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APPLICANT: Innes, Michael
APPLICANT: Teasey, Abla
TITLE OF INVENTION: Production of Tissue Factor Pathway
TITLE OF INVENTION: Inhibitor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZUP: 9460 8.50 ZUP: 9660 8.50 ZUP: 9
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Pred. No. 4.1e-07;
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                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Domain
LOCATION: 189..239
CONTER INFORMATION: /Label- Kunitz-3
US-08-796-850-1
                                                                                                                                                                                                                                                                                    /label- Kunitz-2
                                                                                                                                                            /label- Kunitz-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08854764
Patent No. 6103500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/POCKET NUMBER: 09:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0%;
Matches 18; Conservative (
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CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                           NAME/KEY: Domain
LOCATION: 26..76
OTHER INFORMATION:
                                                                                                                                                                                                                                                       LOCATION: 97..147
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                      NAME/KEY:
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                                                             FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INEGRATION:
APPLICANT: Papathanassiu, Adonia E
APPLICANT: Green, Shawn J.
TITLE OF INVENTION: Compositions and Methods for Inhibiting
TITLE OF INVENTION: Cellular Proliferation
                                Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
NAME/KEY: Active-site
LOCATION: 167.168
OTHER INFORMATION: /note= "Potential site for N-linked
OTHER INFORMATION: glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Active-site
LOCATION 117.118
OTHER INFORMATION: /note= "Potential site for N'linked
OTHER INFORMATION: glycosylation"
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,850
                             Score 96; DB 1;
Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Site of partial phosphorylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08796850
Patent No. 5981471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamle L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKEY NUMBER: 0521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                             100.08;
                                                                                                                                                  DSEEDEEHTIITDTELPP 18
                                                                                                                                                                                         1 DSEEDEEHTIITDTELPP 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 amino acids
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                                                             Local Similarity 100.
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228..229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 2..3
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georgia
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: NORIGINAL SOURCE:
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LOCATION:
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Search completed: September 20, 2002, 10:27:39
Job time: 22 sec
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US-08-943-682-9
                                                                                                                                                                                                                           ; MOLECULE TYPE:
US-08-943-682-9
                                                                                                                                             Query Match

Best Local Similarity

Matches: 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08943682 Patent No. 6174721
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                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 08/438,184
ETILING DATE: 09-MAY 1995
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY,AGENT INFORMATION:
NAME: Savereide, Paul B
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    TELEFAX: 510-655-3542
NFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT Innis, Michael
APPLICANT Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94608
COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4560 Hort
CITY: Emeryville
STATE: CA
                                                                                                                                                                                                                                                           STRANDEDNESS: 51
                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/943,682 FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DSEEDEEHTIITDTELPP 18
                                                                                                                                                                                                                                                                                                       276 amino acids
                                                                                                                                             Conservative
                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                          single
                                                                                                                                                          100.0%; Score 96; DB 4; 100.0%; Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. 4.1e-07; tive 0; Mismatches 0;
                                                                                                                                              0
                                                                                                                                             Mismatches
                                                                                                                                                                         Length 276;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                             0;
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Resu
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                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GénCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            283138 segs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0:5
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96
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117.182 Million cell updates/sec
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43	43	43	43	43	43	43	43	43	43	43	43	43.5	43.5	44	44	•
44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	45.3	45.3	45.8	45.8	
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A45493	A41618	A39299	S40243	T30901	T18222	JC5757	S25541	A43289	A31555	D69037	S68257	JC4889	T27427	S03170	T48079	
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phospholipase C-be	DNA-directed DNA p	DNA-directed DNA p	DNA-directed DNA p	cyclic nucleotide	DNA polymerase del	DNA-directed DNA p	heat shock protein	CDC4L protein - hu	interferon gamma r	PET112-like protei	phospholipase C (E	phosphatidylinosit	hypothetical prote	homeotic protein c	hypothetical prote	

### ALIGNMENTS

cal number of	hits se	ıtisfying	chosen p	hits satisfying chosen parameters:	283138	
imum DB seq imum DB seq	length: length:	2000000000	8	·		•
rt-processing:	;: Minimum Maximum Listing	Match Match first	0% 100% 45 summaries	ies	.*	
abase .	PIR_71:* 1: pir1: 2: pir2: 3: pir3: 4: pir4:	71:* pir1:* pir2:* pir3:* pir4:*				
Pred. No. score gre and is de	No. is the ni greater than derived by	o. is the number of preater than or equal derived by analysis	res l to	predicted by score of the total score di	chance to have a result being printed, stribution.	
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NO Score	Query Match I	Length DB	Ħ		ptio	
2 1 96 90	100.0	304 1 304 1	TIHUGK		tissue factor path	
4 3 56	7.8	1770 2 2225 2	S56221		etical p	
5 - 51	53.1	873 2	JC4863	•	4	
7 50.5	52.6	1256 2	JE0209		homeobox protein Z brain-specific and	
9 49	51.0 50.0	590 2 1085 2	A40437 S55352		glutamic acid-rich	
10 , 47.5	49.5	1221 2	A49457		fibulin-2 precurso	
12 47	49.0		\$69063		probable membrane	
14 46	47.9	2670 2	A01209		N-acetylmuramoy1-L inositol 1,4,5-tri	
15 45 16 45	46.9	244 2 259 1	T20784 B70314		hypothetical prote citrate synthase -	
17 45	46.9		148722		zinc finger protei	
4.			A72087		conserved hypothet	
_	•	5 5	I48724		zinc finger protei	
22   44.5	46.4	•	T21972		hypothetical prote	
-	n isi	106 2	T04032		hypothetical prote	
25 44	45.0	379 2	E69824		two-component sens	
-	, S		JX0334		.P450	
28 44	45.8	888 2	A55318		serine/threonine p	
29 44	45.8	888 2	JC5399		dual leucine zippe	

A;Molecule type: protein
A;Residues: 'XX',31-53,'X',55-56 <GI3>
A;Esperimental source: recombinant material from mouse Cl37 cells
R;Girard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, K.M.; Broze Jr.,
Biochem. J. 270, 621-625, 1990

A; Accession: B60433

A; Molecule type: mRNA

Residues: 1-304 <GI2>

Status: not compared with conceptual translation

A; Experimental source: endothelial cells

A;Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associa A;Reference number: A60433; MUID:89388722 A;Accession: A60433

A;Cross-references: GB:J03225; NID:g180545; PIDN:AAA52022.1; PID:g180546
A;Note: part of this sequence, including the amino end of the mature protein, was con
R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr.,
Thromb. Res. 55, 37-50, 1989

A;Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated A;Reference number: A28650; MUID:88198127 A;Accession: A28650

Molecule type: mRNA Residues: 1-304 <WUN>

A;Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibit A;Reference number: S13034; MUID:91054349
A;Accession: S13034

ype: protein 29-35 <GI4>

J. Biol. Chem. 263, 6001–6004, 1988  A:Title: Cloning and Characterization of a cDNA coding for the lipoprotein-associated
R; Wun, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
A;Cross-references: GB:M58650; GB:J05312; NID:g186827; PIDN:AAA59480.1; PID:g186829.
A; Residues: 1-304 <van></van>
A; Molecule type: DNA
A; Accession: A39176
A; Reference number: A39176; MUID: 91129227
A; Title: Intron-exon organization of the human gene coding for the lipoprotein-associ
Biochemistry 30; 1571-1577, 1991
R; van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.
A;Cross-references: GB:M59493; GB:M59499; NID:g187204; PIDN:AAA59526.1; PID:g187206
A; Residues: 1-304 <gir></gir>
A; Molecule type: DNA
A; Accession: A23712
A; Reference number: A23712; MUID: 91161593
A; Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. In
J. Biol. Chem. 266, 5036-5041, 1991
R; Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers, M
C; Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A38294; S03903
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
C; Species: Homo sapiens (man)
N; Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation in
tissue factor pathway inhibitor precursor [validated] - human
TIHUGK
ZESOLL L

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Conservative
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F:135/Inhibitory site: Arg (coagulation factor X) #status experimental
F:45,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:227/Inhibitory site: Arg (unidentified proteinase) #status predicted
                                                             Biol. Chem. 264, 18832-18837, 1989
Title: Purification and characterization of the lipoprotein-associated coagulation inf
Reference number: A34315; MUID:90036996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Girard, T.37; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.; ture 338, 518-520, 1989

ture 338, 518-520, 1989

trile: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-as Reference undber: S03993: MUID:89181950

Contents: annotation; site-directed mutagenesis

Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
                                                                                                                                                                                                                                                                                                                                                        edersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K. Mole. 265, 16786-16793, 1990
Miol. Chem. 265, 16786-16793, 1990
Lile: Recombinant human extrinsic pathway inhibitor. Production, isolation, and chara
eference number: A38294; MUID:91009092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ords: anticoagulant; blood coagulation; animal Kunitz-type proteinase inhibitor
/Domain: signal sequence fstatus predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Binding site: phosphate (Ser) (covalent) *status experimental
-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scription: regulates clotting by factor Xa-dependent inhibition of the coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304/Product: tissue factor pathway inhibitor estatus experimental da 104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>5-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>-267/Oomain: animal Kunitz-type proteinase inhibitor homology <BP3>-267/Oomain: animal Kunitz-type proteinase inhibitor homology <BP3>
W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-289/Region: heparin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p position: 2q32-2q32
trons: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1
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                                                                                                                                                                                                                                  Molecule type: protein
Residues: 'XX',31-33,'L',35-50 <NOV>
Experimental source: plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lecule type: protein
                                                                                                                                                                                       Accession: A34315
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Gaps
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Length 304;
                   Indels
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Score 96; DB 1;
Pred. No. 2.7e-07;
                   Mismatches
100.0%;
100.0%;
                  Conservative
       Local Similarity
                  18;
Query Match
                  Matches
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Gaps

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Length 1770;

DB 2;

Score 56; Pred. No.

58.3%;

# DSEEDEEHTIITDTELPP 46 1 DSEEDEEHTIITDTELPP 18

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59 윱

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C;Accession: JC2264
R;Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamot J Blochem. 115, 708-714, 1994
A;Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path A;Reference number: JC2264; MUID:94375417
                                   N'Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coage
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
factor pathway inhibitor precursor
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coagulation inhit

A, Cross-references: GB:S73337; NID:g685016; PIDN:AAB31955.1; PID:g685017 A; Residues: 1-304 <KAM> Molecule type: mRNA A; Accession: JC2264

C.Comment: This protein inhibits the activities of factor Xa and tissue factor-factor vi C.Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor C.Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor

Experimental

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F;29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;24-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;155-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status pred F;135/Inhibitory site: carbohydrate (Asn) (covalent) #status predicted F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, May 1995
A; Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces
A; Reference number: $56186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: D50617; NID: 9836685; PIDN: BAA09206.1; PID: d1009846; PID: 9836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 29-Oct-1999
R;Murakani, Y:: Natt...
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Pred. No. 2.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.8%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DSEEDEEHTIITDTELPP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1770 <MUR>
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PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3 Species: Caenorhabditis elegans Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999 hypothetical protein W01F3.3 - Caenorhabditis elegans A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA Cispecies: Caenorhabditis elegans Cibate: 15-Oct-1999 #sequence\_revision 15-Oct-1 CiAccession: T26063 R;Cummings, P. Submitted to the EMBL Data Library, March 1997 A;Cross-references: EMBL:292815; Pi A:Experimental source: clone WOlF3 A; Reference number: Z20145 A; Accession: T26063 A; Residues: 1-2225 <WIL>

525/3; 774/1; 1093/1; 1178/1; 1221 Length 2225; A;Map position: 5 A;Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 5 DB Score 55; 57.3%; Query Match

A; Gene: CESP: W01F3.3

Genetics

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                                                                                                                                                                                                                                                                                                                                                          omeobox protein ZHX1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:254200; NID:g2687851; PIDN:CAA90905.1; PID:
Comment: This protein belongs to zinc-finger class of homeodomain;
Superfamily: unassigned homeobox proteins; homeobox homology
                                                                       Superfamily: unassigned homeobox proteins; homeobox homology keywords: bone; DNA binding; homeobox; nucleus; transcription regulation; zinc; 10-93/Region: zinc finger
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285-341/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (man);Date: 03-Dec-1999 #text_change 21-Jul-2000
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternate
                                                                                                                                                                                                                                                             Title: Human ZHX1: Cloning,
                                                                                                                                                                                                                                                                                               Yamada, K.; Printz, R.L.; Osawa, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
             465-521/Domain:
569-625/Domain:
                                          102-125/Region:
285-341/Domain:
                                                                                                                                       Gene: zhxl
                                                                                                                                                      Genetics:
                                                                                                                                                                   Cross-references: GB:AF106862; NID:g5757883; Experimental source: liver
                                                                                                                                                                                                    Residues: 1-873 <YAM>
                                                                                                                                                                                                                    Molecule type: mRNA
                                                                                                                                                                                                                               Reference number: JC7079; Accession: JC7079
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70-93/Region:
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Biophys. Res. Commun. 224, 870-876, 1996
zhx-1: A novel mouse homeodomain protein containing two zinc-fingers and five chx-1: A novel mouse homeodomain protein containing two zinc-fingers and five charge number: JC4863; MUID:96311380
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s: homeodomain-containing protein zhx-1
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homeobox homology <HOX2>
homeobox homology <HOX3>
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             homeobox homology
                                            homeobox homology
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                                                         finger
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Pred. No.
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             <HOX2>
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                                            <HOX1>
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<HOX4>
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4-621, 1999
                                                                                                                                                                                                                                                                location,
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C; Date: 21-
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                                                                                                                                                                                                                                                                            R; Sugimoto, Y.; YE Proc. Natl. Acad.
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                                                                                        Query Match
Best Local Si
Matches 7;
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A; Molecule type: mRNA
A; Residues: 1-1256 <SHI>
A; Cross-references: GB: Ai
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A;Title: Cloning and characterization of BAI-associated protein 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;741-765/Region: arginine/glycine-rich F;771-827/Domain: homeobox homology <HO
                                                                                                                                                                                                                     glutamic acid-rich protein, retinal - L
C;Species: Bos primigenius taurus (catt
C;Date: 14-Feb-1992 #sequence_revision
C;Accession: A40437
                                                                                                                                         A; Reference number: A40437; A; Accession: A40437
                                                                                                                                                                      Proc. Natl. Acad. Sci. U
A; Title: The amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;359-396/Domain: WW repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
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N;Alternate names: BAI1-associated protein 1; BAP1
                                                                                            Molecule type: mRNA
Residues: 1-590 <SUG>
                                                                                                                          Status: preliminary
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Best Local Similarity
Matches 11; Conserv
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21-Aug-1998 #sequence_revision 21-Aug-1998
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Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AB010894; NID:g3370997 ce: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDB:9864783
                                                                            GB:M61185; NID:g163077; PIDN:AAA30536.1;
                                                                                                                                                                                       ami, K.; Tsı
U.S.A. 88,
                                                                                                                                                                          sequence of
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61.1%;
              51.0%;
38.9%;
                                                                                                                                                        uence of a glutamic
MUID:91195303
                                                                                                                                                                                                                                                                     retinal - bovine
                                                                                                                                                                                                                                                                                                                                                      270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  861
                                                                                                                                                                                                        Tsujimoto,
                                                                                                                                                                                                                                                                                                                                                                                                                   2
              Score 49; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51;
                                                                                                                                                                                       jimoto, M.; Khorana,
3116-3119, 1991
                                                                                                                                                                                                                                                        (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <HOX5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                       14-Feb-1992 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
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                                                                                                                                                                          acid-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein 1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ?
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 4
                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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                             Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1256;
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Indels
                                                                                                                                                                                                         H.G.;
                                                                                                                                                                          protein
                                                                             PID:g163078
                                                                                                                                                                           from bovine retina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _Gaps
 Gaps
 0;
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Status: nucleic acid sequence not shown

Accession: S55352

.; Thurlaux, P.

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A.Molecule type: protein
A.Residues: 25-33, "X', 35-46 <COL>
C.Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibit
C.Seywords: anticoagulant; glycoprotein
F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
                                                                                                                          ξ.
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the extended form of an endothelial
                                                                                                                          coagulation inhibitor; endothelial cell tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                 coagulation inhibitor
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C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 06-Feb-1998
                                                                                                                                                                C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Saccharomyces cerevisiae)
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                                                                                        rabbit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 300;
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A; Description: The sequence of S. cerevisiae cosmid 9513.
A; Reference number: S69057
                                                                                                                                                                                                                                       C; Accession: S12143; A61373
R; Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
Nucleic Acids Res. 18, 6440, 1990
A; Title: CDNA sequence of rabbit lipoprotein-associated A; Reference number: S12143; WUID:91057146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.
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Pred. No. 11;
2; Mismatches
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96-112/Domain: transmembrane #status predicted
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Colburn, P.; Crabb, J.W.; Buonassisí, V. J. Cell. Physiol. 148, 320-326, 1991
J.*Telle: Enhanced inhibition of tissue factor A;Reference number: A61373; MUID:91349227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable membrane protein YPR075c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.08;
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318 DEDDDEEGSFILDLEIP 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AEEDEEFTNITDIKPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity.
Matches 10; Conserva
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A; Residues: 1-360 <COU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -300 <WES>
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                                                                                                                                                                                                                               aast 11, 261-270, 1995
Title: The IFH1 gene product interacts with a fork head protein in Saccharomyces cerev
Reference number: S55352; MUID:95304839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:X75285; NID:g437046; PIDN:CAA53040.1; PID:g437047
Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.
1r. J. Blocchem. 240, 427-434, 1996
Ir. J. Blocchem. 240, 427-434, 1996
Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix met Reference number: S74094; MUID:96439073
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Keywords: calclum binding; duplication; extracellular matrix; glycoprotein; homotrimer
F; 942-978/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                   C;Species: Sadcharomyces cerevisiae
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: S55352; S51446; S47477
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 11-Jan-2000
C;Accession: A49457; S74095
R;Pan, T.C.; Sagaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
Residues: 1,213085 <CHE>
Cross-references: EMBL: 229488; NID:9531491; PIDN:CAA82624.1; PID:9531492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:U19027; NID:g609363; PID:g609372; MIPS:YLR223c
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Title: Structure and expression of the structure and expressio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description: The sequence of S. cerevisiae cosmid 8083. Reference number: S51443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB.;
Pred. No. 35;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47.5; DE Pred. No. 48; 4; Mismatches
st (Saccharomyces cerevisiae)
protein L8083.9; protein YLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Gene: SGD:IFH1; RRP3
A:Cross-references: SGD:S0004213; MIPS:YLR223c
A:Map position: 12R
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50.0%; illarity 47.1%; Conservative

Query Match Best Local Similarity 8; Conserve

Molecule type: DNA Residues: 1-1085 <HAL>

à 8 - mouse

fibulin-2 precursor

A; Molecule type: mRNA A; Residues: 1-1221 <PAN> preliminary

274 DEEEEEETLVTE---PP 288

ò 셤

Query Match Best Local Similarity

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Science 294, 849-852, 2001
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: MD1209
A;Accession: MD1209
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A46719
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Best Local Similarity
Thes 8; Conserv
                                                                                                  hypothetical protein F11D11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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Best Local Similarity
Thes 7; Conserve
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J. Biol. Chem. 268, 11356-11363, 1993
A;Title: Sequence and functional characterization of a third inositol trisphosphate receptare number: A46719; MUID:93266594
A;Status: A46719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords:
                                        submitted to the EMBL Data Library, November 1996
                                                              R; Mortimore, B.;
A;Reference number:
A;Accession: T20784
                                                                           C; Accession:
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A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nositol 1,4,5-trisphosphate receptor subtype 3 - rat
;Species: Rattus norvegicus (Norway rat)
;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
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;Date: 27-NOV-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2001
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Residues: 1-572 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: nucleic acid Residues: 1-2670 <BLO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
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                                                              Basham, V.
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Pred. No.
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                                                                                                    15-Oct-1999 #text_change 15-Oct-1999
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Wehland,
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A; Gene: CESP:F11D11.7
A; Map position: 5
A; Introns: 90/3; 185/1; 212/3
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A; Residues: 1-244 <WILD
A; Cross-references: EMBL: Z81500; PIDN: CAB04102.1; GSPDB: GN00023; CESP: F11D11.7
A; Experimental source: clone F11D11
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                                            Query Match
Best Local Similarity
Thes 8; Conserve
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78 ESDRSEEHYVAIKTELP 94
                            1 DSEEDEEHTIITDTELP 17
                                                            Conservative
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Pred. No. 17;
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Search completed: September 20, 2002, 10:28:02 Job time: 45 sec

US-08-276-224-10
US-08-279-753-10
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3 US-09-924-340-94
3 US-10-000-489-94
4 US-10-000-986-94
4 US-10-000-986-94
5 US-09-94-590-96
5 US-09-94-590-96
6 US-10-000-489-96
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Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 94, Appl Sequence 94, Appl Sequence 94, Appl Sequence 94, Appl Sequence 96, Appl

116, Appli 116, App 116, App 116, Appli e 1, Appli e 48, Appli e 52, Appli

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Scoring table:
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Sequence 7, Application US/08286530 GENERAL INFORMATION: APPLICANT: Innes, Michael APPLICANT: Creasey, Abla TITLE OF INVENTION: Production of Tissue Factor Pathway TITLE OF INVENTION: Inhibitor NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSEE: Chiron Corporation STREET: 4560 Horton St. CITY: Emeryville STATE: CA COUNTRY: USA ZIT: 94608 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION NUMBER: US/08/286,530 FILING DATE: 05-AUG-194 CLASSIFICATION NUMBER: US/08/286,530 FILING DATE: 05-AUG-194 CLASSIFICATION NUMBER: 0991.001 REFERENCE/DOCKET NUMBER: 36,914 REFERENCE/DOCKET NUMBER: 0991.001 TELECOMMUNICATION INFORMATION:	96 100.0 276 21 US-09-741-106-9 96 100.0 276 21 US-09-766-778-1 96 100.0 291 23 US-09-924-340-48 96 100.0 291 23 US-09-924-340-52 96 100.0 291 23 US-09-994-590-48 96 100.0 291 23 US-09-994-590-48 96 100.0 291 24 US-10-000-489-48 96 100.0 291 24 US-10-000-489-52 96 100.0 291 24 US-10-000-986-52 96 100.0 291 26 US-60-305-456-48 96 100.0 291 26 US-60-305-456-48 96 100.0 304 4 US-08-026-146-2 96 100.0 304 5 US-08-179-660-23 96 100.0 304 10 US-08-264-272-16 96 100.0 304 11 US-08-264-272-16	9 96 100.0 164 24 US-10-000-986-96 9 96 100.0 164 26 US-60-305-456-96 1 96 100.0 210 4 US-80-305-126-18 S 2 96 100.0 276 4 US-08-085-126-116 S 3 96 100.0 276 6 US-08-286-530-3 S 4 96 100.0 276 8 US-08-286-530-3 S 96 100.0 276 8 US-08-438-114-116 S 96 100.0 276 16 US-09-130-273-1 S 96 100.0 276 16 US-09-265-468-1
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APPLICANT: JOBET, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFRENCE: 81.0S1.PRO
CURRENT PILLING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.951.PRO
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Pred. No. 2.4e-07;
Mismatches 0;
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Pred. No.
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                          PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 18388
LENCTH: 66
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Matches 18; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Tanaka, Hiroaki,
APPLICANT: Tanaka, Hiroaki,
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTs and Encoded Human Proteins
FILE REFERENCE: 81.052.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF ENVENTION: ESTS and Encoded Human Proteins
FILE REFERENCE: 81.082.REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR PILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18388, Application US/09834366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09834366
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100.0%; Pr
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                                                                                                                                                                                                                               Query Match
Best Local Sindarity 100.0%;
Matches 187 Conservative 0
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   510-601-2585
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                          TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTHAT 118 imino acids
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                        single
                                                                                                                                                   MOLECULE TYPE: peptide us-08-286-530-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                       linear
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NAME/KEY: UNSURE
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TELEPHONE:
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NUMBER OF SEQ ID NOS: SOFTWARE: Patent.pm SEQ ID NO 18386

52153

ENGTH:

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; LOCATION: -28..-1
US-09-834-366-13738
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; LOCATION: -28..-1
US-60-197-873-18388
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Best Local S
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent.pm
SEQ ID NO 13738
LENGTH: 79
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Sequence 13738, A
                                       FILE REFERENCE: 81.US1.PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT; APPLICATION NUMBER: US/09/834,366
                                                                                                      PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/197,873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT: Bejanin, Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo saplens
                                                                                                                               PPLICANT:
                                                                                                                                                             PPLICANT
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                                                                                                                                                 PPLICANT:
                                                                                       TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 DSEEDEEHTIITDTELPP 46
                                                                                                                                                                                                                                                                                                                                       Local Similarity
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: Patent.pm
13738
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                                                                                                   Giordano,
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                                                                                                                                                                                       Application US/60197873
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                                                                                                                                              Hiroaki
                                                                                     ESTs and Encoded Human Proteins.
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                                                                                                   Jean-Yves
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100.0%; Pred. No. 3
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; LOCATION: -28..-1
US-60-197-873-13738
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Best Local Similarity
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                                                                                TELEFAX: 212 867 0298 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/DK92/00340 FILING DATE: 16-NOV-1992 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/I
FILING DATE: 07-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                             FILING DATE: 22-FEB-1993 ATTORNEY/AGENT INFORMATION:
 OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
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                 TOPOLOGY: linear
                                                                                                                                             NAME: Lowney, Karen A. REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/DK93/00005
FILING DATE: 07-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 15-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Novo Nordisk of North America, 405 Lexington Avenue, Suite 6400
                                              132 amino acids
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Norris, Kjeld
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
protein
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                                                                                                                                                                                                                              US 08/021,605
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                                                                                                                                                             31,274
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Pred. No. 3.1e-07;
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Matches

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APPLICANT: Petersen, Lars Christian
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: A Human Kunitz-Type Protease Inhibitor
TITLE OF INVENTION: Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,753A
FILING DATE: 21-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                      E: Novo Nordisk of North America, Inc
405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00002
FILING DATE: O7-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00340
FILING DATE: 16-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK93/00005
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,605
FILING DATE: 22-FEB-1993
ATTORNEY AGGNT NUMBER: US 08/021,605
FILING DATE: 22-FEB-1993
ATTORNEY AGGNT NUMBER: US 08/021,605
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Application US/08279753A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REPERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION
TELEPHONE: 212 867 0123
                                                                      Norris, Kjeld
Bjorn, Soren Erlk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DSEEDEEHTIITOTELPP 18
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TYPE: amino acid
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTY: U.S.A..
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 867 0298
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                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-924-340-94
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                                                                      Gaps
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Variant
                        100.0%; Score 96; DB 6; Length 132; 100.0%; Pred. No. 6e-07;
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COMPUTER: IBM PC compatible
OPERATING SSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,753
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00002
FILING DATE: 07-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00340
FILING DATE: 16-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK93/00005
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK93/00005
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
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                                                                      Indels
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                                                                                                                                                                                                                                                                               Application US/08279753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lowney, Raren A. REGISSTRATION NUMBER: 31,274 REFERENCE/DOCKET NUMBER: 36 RELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                 1 DSEEDEEHTIITOTELPP 18
                                                                                                                                            54 DSEEDEEHTIITDTELPP 71
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                                         Local Similarity 100.
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A TITLE OF INVENTION: VA NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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ZIP: 10174-6401
COMPUTER READABLE FORM:
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GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                        Query Match
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APPLICANT: Belania.
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF.
FILE REFERENCE: 91.032.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
Length 132;
                                             Indels
100.0%; Score 96; DB 6; 100.0%; Pred. No. 6e-07;
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RESULT 10 US-08-279-753A-10

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APPLICATION NUMBER: US 60/305,456 FILING DATE: 2001-07-13

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; LOCATION: 1..19
US-09-924-340-94
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Best Local :
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                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US:60/305,456
PRIOR FILING DATE: 2001-07-13
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                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/IB01/01715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                   NAME/KEY: SIGNAL
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/302,277
                                                                                                                                                                                                                                                                           PLICATION NUMBER: US 60/293,574
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PRIOR FILING DATE: 2001-08-06
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NAME/KEY: SIGNAL OCATION: 1..19
                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/305,456
FILING DATE: 2001-07-13
APPLICATION NUMBER: US 60/302,277
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FILING DATE: 2001-08-06
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                                                                                                                                                       APPLICATION NUMBER: US 60/293,574 FILING DATE: 2001-05-25
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Pred. No.
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    Length 152;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
      100.0%; Score 96; DB 24; 100.0%; Pred. No. 7.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/741,106
FILING DATE: 12-Dec-2000
CLASSIFICATION AURONN
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/286,521
FILING DATE: 1994-08-05
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELEPHONE: 510-651-2585
TELEPHONE: 510-651-2585
INFORMATION FOR SEQ ID NO: 19:
                                                    Mismatches
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TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDMESS: single
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-741-106-19
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
                                                                                                                                                                                                           S-09-741-106-19, Sequence 19, Mapplication US/09741106
GENERAL INFORMATION:
APPLICANT: Innis, Michael
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LENGTH: 161 amino acids
TYPE: amino acid
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                                                                                         1 DSEEDEEHTIITOTELPP 18
                                                                                                                 Query Match FFF 100. Best Local Similarity 100. Matches 18; Conservative
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100.0%; Score 96; DB 21; Length 161; 100.0%; Pred. No. 7.8e-07;

Query Match Best Local Similarity Matches 18; Conserv

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Search completed: September 20, 2002, 10:30:30 Job time: 193 sec

Indels

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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US-09-791-537-76349
US-09-791-537-107368
US-10-104-047-3582
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US-10-206-272-546
US-10-206-272-547
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US-09-992-600A-96
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Sequence 96,
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                        50, Appl 142737, 76349, 76349, Ap 3582, Ap 205, App 1623, Ap 108592, 108592,
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547, App
7632, Ap
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39142, A
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120691,
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15150, A
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101054,
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US-09-992-600A-96
US-09-992-600A-96
Sequence 96, Application US/09992600A
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
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45.8	45.8	45.8	45.8	45.8	46.4	46.4	46.9	46.9	46.9	46.9	46.9	46.9	46.9	47.9	47.9	4.7.9	49.0	49.0
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US-09-791-537-6416	US-10-155-881-31345	US-10-155-881-21041	US-10-155-881-18133	US-10-212-778-761	US-60-360-039-16039	US-60-360-039-15654	US-09-458-180-2	US-10-106-698-4636	US-10-067-741-7	US-09-791-537-131924	US-10-155-881-10994	US-09-791-537-118383	US-10-155-881-22243	US-10-179-131-8354	US-10-179-131-8385	US-10-008-524A-153	US-09-791-537-68627	US-09-791-537-11292
Sequence 6416,	Sequence 31345	Sequence 21041	Sequence 18133	Sequence 761,	Sequence 16039	Sequence 15654	Sequence 2, Ap	Sequence 4636,	Sequence 7, Ap	Sequence 13192	Sequence 10994	Sequence 11838	Sequence 22243	Sequence 8354,	•		Sequence 68627	Sequence 11292
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; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-992-600A-94
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US-09-992-600A-94
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                                                                                                                                                                                                                                                                                                     SOFTWARE: JPatent
SEQ ID NO 94
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
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PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US4.DIV
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                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
Local Similarity nes 18; Conserv
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                                                                                  Conservative
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                                                                                                     100.0%; Score 96; DB 5;
100.0%; Pred. No. 1.6e-06;
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                                                                                    Mismatches
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ositions and Methods for Inhibiting Cellular Proliferation
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APPLICANT: Green, Shawn J
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Prol
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Prol
TITLE OF INVENTION: TEPT Fragments
FILE REFERENCE: 05213-0296 43170-266780
CURRENT APPLICATION NUMBER: US/10/086,176A
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR FILING DATE: 1999-01-11
PRIOR FILING DATE: 1999-01-11
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-02-06
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-08-06
NUMBER: OF SEQ ID NOS: 6
SONTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR FILING DATE: 1999-01-11
PRIOR FILING DATE: 1999-01-11
PRIOR FILING DATE: 1997-02-06
PRIOR FILING DATE: 1997-02-06
PRIOR PILING DATE: 1997-02-06
PRIOR APPLICATION NUMBER: US 09/130,273
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 6
SSOFWARE: Patentin version 3.1
LENGTH: 276
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Pred. No.
                                                                                       FILE REFERENCE: 05213-0296 43170-26780 CURRENT APPLICATION NUMBER: 05/10/086,176 CURRENT FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic peptide US-10-086-176-5
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; OTHER INFORMATION: Synthetic peptide
US-10-086-176A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/10086176A GENERAL INFORMATION:
APPLICANT: Hembrough, Todd
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Best Local Similarity 100.0
Matches 18; Conservative
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Best Local Similarity
Matches 18, Conserva
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATERLIN VERSION 3.0
OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
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                                FILE REFERENCE: 91.054.01V
CURRENT APPLIGATION NUMBER: 05/09/992,600A
CURRENT PILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 15/09/924,340
PRIOR PELING DATE: 2001-08-06
PRIOR PELING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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Best Local Similarity 100.0%;
Matches 18; Conservative (
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US-09-791-537-120691
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US-09-992-600A-96
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LENGTH: 251
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                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/992,600P
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GANISM: Homo sapiens
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APPLICATION NUMBER: PCT/IB01/01715
FILER DATE: 2001-08-06
APPLICATION NUMBER: US 60/305,456
FILING DATE: 2001-07-13
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FILING DATE: 2001-08-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                        52, Application US/09992600A INFORMATION:
                                                                                            OF SEQ ID NOS: 114
                                                                                                                                                                                           PPLICATION NUMBER: US 60/302,277
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Conservative (
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Pred. No.
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CURRENT FILING DATE: 2002-06-11
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                            APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
FILE REFERENCE: DYX-007.2P US-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/791,537
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/638,770
                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION
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                                                                                                                                                                          R FILING DATE: 2000-08-15
                                                                                                                                         FILING DATE: 1999-10-08
                                                                                                                       APPLICATION NUMBER: 09/240,136
                                                                                                                                                      APPLICATION NUMBER: 09/414,878
FILING DATE: 1994-03-10
              APPLICATION NUMBER: 08/208,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -537-101054
                                                                                    APPLICATION NUMBER: 08/676,124
                                               APPLICATION NUMBER: PCT/US95/00298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101054, Application US/09791537
                                                                   LING DATE: 1997-01-07
                                 LING DATE: 1995-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                   Application US/10167351
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Pred. No. 3
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 304;
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                  equals any of the naturally occurring L-amino acids
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Pred. No. 0.0004;
); Mismatches 0;
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CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 09/758,445
PRIOR PELING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
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Best Local Similarity 100.0%;
Matches 15; Conservative (
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NUMBER OF SEQ ID NOS: 816
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 547
LENGTH: 103
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                                                                                                                                                                                  OTHER INFORMATION: Xaa
                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (78)
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                    Length 304;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PMO27CIN
CURRENT APPLICATION NUMBER: US/10/206,272
GURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 09/758,445
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-13
PRIOR PILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTU
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 15150
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Local Similarity 100.0%;
les 18; Conservative C
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 546
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Best Local Similarity 94.4
Matches 17; Conservative
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US-09-791-537-15150
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bionomix, Inc
APPLICANT: Debe, Derek
TYPE: PRT ( OKGANISM: Homo saplens US-10-167-351-1 ( )
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Matches
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US-10-206-272-547

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                                                                               ORGANISM: Homo sapiens
JS-10-211-346-468
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LENGTH: 434
TYPE: PRT
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Best Local Similarity 55.6
Matches 10; Conservative
Query Match
Best Local Similarity
Matches 11; Conserv
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                            SEQ ID NO 468
                                                                                                                                                                                                                                                                                                                                                                  Sequence 468, Application US/10211346 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Candida albicans
                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: 09/758,469
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
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CURRENT FILING DATE: 2002-06-21
                                                                                                                                                             SOFTWARE: PatentIn Ver.
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ITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES,

ITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                               ENGTH: 100
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                                                                                                                                                                                                                                                                                                                       REFERENCE: PM008C1N
                                                                                                                                                                                                           APPLICATION NUMBER: 60/180,628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HARE, ROBERTA S.
SHAW, KAREN J.
SHIMER JR., GEORGE H.
KESSLER, MACCO
NOLLING, JORK
ZENG, QIADDONG
                                                                                                                                                                                                                                                                                                                                                     Rosen et al.
    Conservative
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                  Pred. No. 4
                                 Score 51; DB 6; Length 100;
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6.3;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 39142
LENGTH: 873
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-39142
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US-09-791-537-39142
Search completed: September 20, 2002, 10:31:44
Job time: 242 sec
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
                                                                                                844 DQEEDEEETDDSDTWEPP 861
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Pred. No. 56;
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                                                                                                                                                                            6; Indels
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Scoring table:
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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CNG4_BOVIN
IFH1_YEAST
FBL2_MOUSE
TFPI_RABIT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPOPROTEINS IN PLASMA.

-1- SUBCELLULAR LOCATION: Secreted.
-1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha/TFPIalpha (shown here) and beta/TFPIbeta; are produced by alternative splicing.
-1- TISSUB SPECIFICITY: MOSTLY IN ENDOTHELIAL CELLS.
-1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
-1- FIM: O-GLYCOSYLATED.
-1- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                       "Amino acid sequence and carbohydrate structure of a recombinant human tissue factor pathway inhibitor expressed in Chinese hamster ovary cells: one N-and two 0-linked carbohydrate chains are located between Kunitz domains 2 and 3 and one N-linked carbohydrate chain is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Broze G.J. Jr., Girard T.J., Novotny W.F.; "Regulation of coagulation by a multivalent Kunitz-type inhibitor."; Blochemistry 29:7539-7546(1990).
                                                                                                                                         [8]
INHIBITORY SITES.

INHIBITORY SITES.

GIATAT G.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G.,
Milettch J.R., Broze G.J. Jr.,

**Function** significance of the Kunitz-type inhibitory domains of lipoprofein-associated coagulation inhibitor.";
                                 25 SEOURINGE OF 29-50.
MEDLINE-REVG36996; PubMed-2553722;
MOVOCHY W.R., Glrard T.J., Miletich J.P., Broze G.J. Jr.;
NOVOCHY W.R., Glrard T.J., Miletich J.P., Broze G.J. Jr.;
"Purification and characterization of the lipoprotein-associated coagulation inhibitor from human plasma.";
J. Biol. Chem. 264:18832-18837(1989).
                                                                                                                                                                                                                                                                                          CARBOHYDRATE-LINKAGE SITES.
MEDLINE-96224851; PubMed-8639592;
Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,
Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91104709; PubMed-2271516;
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AAA59526.1;
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EMBL; M59499; 1
EMBL; M59493; 1
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EMBL; M58647;
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N-LINKED (GLCNAC. ..).
EFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGC
G -> VYKEGTYDGWKNAAHYQVFLNAFCIHASMFFLGLD
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MISSING (IN ISOFORM BETA).
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X(A)
VII(A)/TF.
                                                                                                                                                                              PROSITE; PS00280; BPTL_KUNITZ_1; 3.
PROSITE; PS50279; BPTL_KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation; Signal; Alternative splicing; 3D-structure; Polymorphism.
1 28
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BPTI/KUNITZ INHIBITOR 2
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R->L: ABOLISHES INHIBITION OF
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                                                                                                                                           InterPro; IPR002223; Kunitz_BPTI
PRAM; PR00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
SMART; SM00131; KU; 3.
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TISSUE-Liver;
MEDLINE-94975417; PubMed-8089087;
Kamakkubo Y., Hamuro T.,
Kamel Sker Kamakkubo S., Funatsu
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between
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"Amino acid sequence and inhibitory activity of rhesus monkey
factor pathway inhibitor (TFPI): comparison with human TFPI.";
J. Biochem. 115:708-714(1994).
-1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-D
WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY
A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WI
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Pfam; | PF00014; Kunitz_BPTI; 3.
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HSSP; P10646; 1TFX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPOPROTEINS IN PLASMA.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
PTM: O-GLYCOSYLATED (BY SIMILARITY).
SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                   SITE
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SM00131; KU; 3.
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BPTI_KUNITZ_2;
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Chordata; Craniata; Vertebrata; Euteleostomi;
  35085
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inhibitor precursor (TFPI) (Li
n inhibitor) (LACI) (Extrinsic
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PREACTIVE BOND (
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TISSUE FACTOR PATHWAY
TNHIBITOR
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REACTIVE BOND
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BPTI/KUNITZ INHIBITOR 3.
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(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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sic pathway inhibitor)
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EMBL; U83459; AAB64
EMBL; AJ001030; CAA
HSSP; Q16539; 1WFC.
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P43565;
01-NOV-1995
Pfam; PF00069; pkinase; 2.
Pfam; PF00072; response_reg;
SMART; SM00013; S_TK_X; 1.
SMART; SM0013; S_TK_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                Reinders A., Buerckert N., Boller T., Wiemken A., de Virgilio C. "Saccharomyes cerevisiae cAMP-dependent protein kinase controls into stationary phase through the Riml5p protein kinase."; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Stimulation of yeast meiotic gene e glucose-repressible protein kinase R Mol. Cell. Biol. 17:2688-2697(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., MEDLINE-97265402; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE-95400292; PubMed-7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein kinase RIM15 OR TAK1 OR YFL033C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Serine/threenine-protein kinase RIM15 (EC 2.7)
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                                                              InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR001789; Response_reg.
InterPro; IPR002290; Ser_thr_pkina
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Sasanuma S.-I., Sasanuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vidan S., Mitchell A.P.;
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STRONG, WITH S.POMBE CI
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                                                                                                                     S0001861; RIM15.
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                                                                                                                                                          BAA09206.1; -. AAB64088.1; -.
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                                                                                                                                               CAA04486.1; -.
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                                                              Ser_thr_pkinase.
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Eki T.;
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Fri

SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL

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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96009859; PubMed=7546742;
Koerschen H.G., Illing M., Selfert R., Sesti F., Williams A.,
Gotzes S., Colville.C., Mueller F., Dose A., Godde M., Molday L.,
Kaupp U.B., Wolday R.S.;
*A 240 Kba protein represents the complete beta subunit of the cyclic
nucleotide-gated channel from rod photoreceptor.";
Neuron 15:627-636(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suginoto 1. Yatsunami R., Tsujimoto M., Khorana H.G., Ichikawa A.; Sugimoto 1. Yatsunami R., Tsujimoto M., Khorana H.G., Ichikawa A.; Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.

1- SUBGILIALIA ENCATIONAL HETEROOLIGOMERIC CHANNELS WITH CNG3.

1- SUBCELLOILAR LOCATION: Integral membrane protein.

1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; CNG4C (SHOWN HERE), CNG4D AND CNG4E, ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR THE MOST FREQUENT FORM (CNG4D-CNG4C:CNG4E - 20:2:1) IN IESTIS.

1- TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96198098; PubMed-8626431;
Blel M., Zong X., Ludwig A., Sautter A., Hofmann F.;
"Molecular cloning and expression of the modulatory subunit of the cyclic nucleotide-gated cation channel.";
J. Biol. Chem. 271:6349-6355(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 1; Length 1770;
Pred. No. 1.5;
5; Mismatches 0; Indels
                                                                                                                                 Transferabe; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DC1064825000FAFF CRC64;
                                                                                                                                                                                                                             RESPONSE REGULATORY
                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
(BY SIMILARITY)
PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. PROSITE; PSQ0108; PROTEIN_KINASE_ST; 1. PROSITE; P$50110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028181; Q28082; Q03861;
01-NOV-1997 (Rel. 35, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                             PROTEIN KINASE
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                                                                                                                                                             Phosphorylation; Melosis.
DOMAIN 794 1254
DOMAIN 1636 1750
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Matches 9; Conservative
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Q28181; Q28
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NP_BIND
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DOMAIN
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MISSING (IN ISOFORM CNG4E).
MISSING (IN ISOFORM CNG4D).
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PROSITE; PS01088; CNMP_BINDING_1; 1.
PROSITE; PS01088; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
Ionic channel; Ion transport; CAMP-binding; Transmembrane; Multigene family; Alternative splicing.

Multigene family; Alternative splicing.

"Transmembrane; Multigene family; Alternative splicing."
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EXTRACELLULAR (POTENTIAL).
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H6 (POTENTIAL)
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A -> T (IN REF. 3).
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CYTOPLASMIC (POTENTIAL).
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CAMP (BY SIMILARITY).
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(Rel. 31, Last sequence update)
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Interpro; IPR000595; CMMP_binding.
Pfam; PF00027; CMMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
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Pred. No.
                                                                                                                                                              EMBL; X89626; CAA61769.1; -.
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Best Local Similarity 38.9.
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01-FEB-1995
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P39520;
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RESULT 6
FBL2_MOUSE
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Best Local
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-I- FUNCTION: CONTROLS THE PRE-RRNA PROCESSING MACHINERY IN CONJUNCTION WITH FHL1. COULD CONVERT FHL1 FROM A REPRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cherel I., Thuriaux P.;
"The IFHI gene product interacts with a Saccharomyoes cerevisiae:";
Yeast 126261-270(1995).
                                                                                              FBL2_MOUSE STANDARD; PRT; 1221 AA p37889; Q9WUI2; 01-OCT-1994 (Rel. 30, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Fibulin-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyco
Saccharomycetales; Saccharomycetaceae; Sac
SEQUENCE FROM N.A., TISSUE-Fibroblast;
                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-10090;
[1]
                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Transcription regulation.

DOMAIN 122 163 ASP/GLU-RICH (HIGHLY ACIDIC).

SEQUENCE 1085 AA; 122491 MW; BE1C7DEF06213FE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 229488; CAA82624.1;
EMBL; U19027; AAB67412.1;
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$0004213; IFH1.
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8; Conserv
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             AND
                                               Rodentia;
                                                            Chordata;
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             SEQUENCE
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Pred. No.
                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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InterPro;
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MGI:95488;
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AF135251;
AF135252;
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AF135249;
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AF135244;
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AF135239;
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use by non-profit institutions as lon modified and this statement is not remove entitles requires a license agreement (5 or send an email to license@isb-sib.ch).
                                                                                                                     This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                              characterization.";
Eur. J. Biochem. 263:471-477(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;
"Mouse fibulin-2 gene. Complete exon-intron organization and Characterity artics."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., MEDLINE-99337686; PubMed-10406956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein with multiple EGF-like repeats and consensus motifs for
                                                                                                                                                                                                         SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: COMPONENT OF BOTH BASEMENT MEMBRANES AND OTHER
                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                      CALCIUM DEPENDENT.
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                                                                                                                                                                                                                                                                                              PRESENCE OR ABSENCE OF A SINGLE ALTERNATIVE SPLICING.
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CAA53040.1;
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                                                                                                                                                                                                                                                                                                                    Extracellular matrix.
AT LEAST TWO FORMS OF
A SINGLE EGF-LIKE (3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Faessler R., Timpl R., Chu M.-L.;
in-2, a novel extracellular matrix
                                                                                                                                                             It is produced through
                                                           (See http://www.
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Pfam; PF01821; ANATO; 2.
Pfam; PF00008; EGF; 6.
SMART; SM00104; ANATO; 3.
SMART; SM00104; ANATO; 3.
SMART; SM00010; EGF_like; 2.
SMART; SM00001; ASX_HYDROXY; 5
Calcium-binding; Alternative SIGNAL. 1 26 CHAIN 27 1221 DOMAIN 27 434 DOMAIN 27 176
                                                                                                                                                                                                                                                                                                                        A49457; A49457.
                                                                     TE; PSO1177; ANAPHYLATOXIN_1; 3
PE; PSO1178; ANAPHYLATOXIN_2; 3
PE; PSO1022; EGF_1; FALSE_NEG.
PE; PSO1186; EGF_2; 5.
PE; PSO1187; EGF_CA; 10.
FG G1yCODTOTOTOTO.
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IPR001881;
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IPR000152;
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EGF_Ca.
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                                                                     Extracellular matrix; Plasma; EGF-like
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                                                    splicing; Repeat.
                             FIBULIN-2
  SUBDOMAIN NA (CYS-RICH).
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domain;

RRROCCOGREGAT

밁 Ş 01-AUG-1992 (Rel. 23, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
11ssue factor pathway inhibitor precursor (TFPI) (Lipoproteinassociated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)

01-FEB-1991 (Rel. 17, Created) 01-AUG-1992 (Rel. 23, Last seq

TFPI\_RABIT P19761; Q28828;

RESULT 7 TFPI\_RABIT

300 AA

Oryctolagus cuniculus (Rabbit). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.

TISSUE-Liver;
MEDLINE-91057146; PubMed-2136251;
Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;
TDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.";

SEQUENCE FROM N.A.

NCBI\_TaxID=9986;

(EPI).

TFPI

Nucleic Acids Res. 18:6440-6440(1990)

Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.; "CDNA sequence of rabbit tissue factor pathway inhibitor."; Nucleic Acids Res. 20:3548-3548(1992).

SEQUENCE FROM N.A

TISSUE-Lung;

MEDLINE-92335027; PubMed-1630940;

REVISIONS TO 72; 211 AND 218

TISSUE-Liver

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EGF-LIKE 2.

EGF-LIKE 3. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11. CALCIUM-BINDING (POTENTIAL).
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CELL ATTACHMENT SITE (POTENTIAL)
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          ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 3.
BARPHYLATOXIN-LIKE 3.
EGF-LIKE 1, CALCIUM-BINDING
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 SUBDOMAIN NB (CYS-FREE).
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5 -> L (IN REF. 2).
7 -> QQ (IN REF. 2).
7 -> E (IN REF. 2).
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Gaps
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Length 1221;
                           Indels
 Score 47.5; DB 1;
Pred. No. 19;
1; Mismatches 2;
   49.5%;
                                                 DSEEDEEHTIITÖTELPP 18
 Query Match 49.5
Best Local Similarity 50.0
Matches 9; Conservative
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BPTI/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
BPTI/KUNITZ INHIBITOR 2
(FACTOR X(A) BINDING SITE). LIPOPROTEINS IN PLASMA.
--- SUBCELLULAR LOCATION: Secreted.
--- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
--- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS. Interpro; IPR002223; Kunitz\_BPTI. Pfam; PF00014; Kunitz\_BPTI; 3. PRINTS; PR00759; BASICPTASE. EMBL; X54708; CAA38515.1; ALT\_SEQ. EMBL; S61902; AAB26836.1; -. PIR; S12143; S12143. HSSP; P10646; ITFX. 24 300 100 171 SM00131; KU; 22 22 121 Signal. SMART; DOMAIN 

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Q63269;
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
101-MAR-2002 (Rel. 41, Last annotation update)
100-MAR-2002 (Rel. 41, Last annotation update)
110-MAR-2002 (Rel. 41, Created)
110-MAR-2002 (Rel. 41, Last sequence update)
110-MAR-2002 (Rel. 41, Last sequ
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This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                             Teticulum (By Similarity).

DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-
EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE
BINDING SITE IN THE N-TERMINUS AND MODULATIORY SITES IN THE
PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.

PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).

SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
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REACTIVE BOND (BY SIMILARITY.

BY SIMILARITY.
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Pred. No.
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receptor isoform
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    ALC REPORT OF THE PROPERTY OF 
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SEQUENCE
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that the
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13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Cytochrome P450 3A1 (EC 1.14.14.1) (CY
                                                                                                                                 STRAIN-WISTAR; TISSUE-Liver; MEDLINE-92117688; PubMed-1731631;
                                                                                                                                                                                                                      Gonzalez F.J., Nebert D.W., Hardwick J.P., Kasper C.B., "Complete cDNA and protein sequence of a pregnenolone 10 carbonitrile-induced cytochrome P-450. A representative
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-85207783; PubMed-3838989;
GONZALEZ F.J., Nebert D.W., Hardw
"Complete cDNA and protein sequen
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InterPro; IPR001682; Channel_pore_Ca_Na.
Burger H.J.,
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                             SEQUENCE OF 1-24 FROM N.A
                                                        "Cloning and characterization of a novel CYP3A1 allelic variant: analysis of CYP3A1 and CYP3A2 sex-hormone-dependent expression rethat the CYP3A2 gene is regulated by testosterone."; arch. Biochem. Biophys. 293:147-152(1992).
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                      Ribeiro V., Lechner
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                              CYP3A1 OR CYP3A-1.
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7; Conserv
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2670
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Schuetz J.D.,
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               PubMed=1372436
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Rodentia;
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Pred. No.
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W; 13C787E4C2886E45 CRC64;
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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E.G.,
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Guzelian P.S.
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                Paradoxical transcriptional activation of rat liver cytochrome P-450
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Microsome; Endoplasmic reticulum; Polymorphism.
                                                                                                                                                 oxidized flavoprotein + H(2)0-1-1 SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
-!- INDUCTION: BY PREGNENOLONE 16-ALPHA-CARBONITRILE (PNCN).
-!- SIMILIBATIV: BELONGS TO THE CYTOCHROME P450 FAMILY.
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F -> I (IN STRAIN WISTAR).
I -> V (IN STRAIN WISTAR).
CFD5AC8C37E9CADB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232
57917 MW;
                                                                                                                                                                                                                                                                                                                                             EMBL; M10161; AAA41035.1; --.
EMBL; X64401; CAA45743.1; --.
EMBL; M86850; AAA41780.1; --.
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232
504 AA;
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ö Gaps ö Score 44; DB 1; Length 504; Pred. No. 24; 4; Indels 5; Mismatches 45.8%; Conservative Query Match Best Local Similarity Matches 7; Conserv

281 DSKDKESHTALSDMEI 296 1 DSEEDEEHTIITDTEL 16 g

01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Heat shock protein 75 km mitochondrial precursor (HSP 75) (Tumor necrosis factor type 1 receptor associated protein) (TRAP-1) (TNFR-01-MAR-2002 (Rel. 41, Created) STANDARD; associated protein 1). musculus (Mouse). TRAL\_MOUSE Q9CQN1; TRAL\_MOUSE
ID TRAL\_MALL
DT OI-MAR
DT 01-MAR
DE HEAT & OI-MAR
DE ASSOCI
GN TRANDING
OC BUKAR
OC MARMIN
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RA RAWAI
RA RAWAI RESULT 10

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musin SEQUENCE FROM N.A.

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., STRAIN-C57BL/6J; TISSUE-Embryonic stem cells, and Kidney; MEDLINE-21085660; PubMed-11217851;

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Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,
Radota K., Matsuda H., Gissi C., King B., Kochiwa H.,
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackehbush J.,
Schrim I. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rabate J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ruonstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee,
Rons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Rusuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Rawaji H., Rohtsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). -i- FUNCTION: Chaperone that expresses an ATPase activity (By Chaperone; ATP-binding; Mitochondrion; Transit peptide. TRANSIT 1 7 7 706 HEAT SHOCK PROTEIN 75 KDA. SEQUENCE 706 AA: 80208 MW; 7183CE538CB36464 CRC64; or send an email to license@isb-sib.ch) PRINTS: PR00775; HEATSHOCK90. SMART; SM00387; HATPASE\_C; 1. PROSITE; PS00298; HSP90; FALSE\_NEG HSSP; PU.300, MOD. MOD. MGD: MGD: J15265; Hrapl. InterPro; IPR003594; HATPase\_C. InterPro; IPR001404; HSP90. EMBL; AK010341; BAB26865.1; -. EMBL; AK002409; BAB22078.1; -. Pfam; PF02518; HATPase\_c; 1. Pfam; PF00183; HSP90; 3. 

ö 45.8%; Score 44; DB 1; Length 706; 53.3%; Pred. No. 35; .ive 4; Mismatches 3; Indels 8; Conservative Query Match Best Local Similarity Matches 8; Conserv

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Gaps

1 DSEEDEEHTIITDTE 15

8

67 DKEEESLHSIISNTE

g

706 AA.

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M3KC\_MOUSE STANDARD; PRT; 888 AA.
060700; P70286;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2002 (Rel. 40, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
M1togen-activated protein kinase kinase kinase Lice (EC 2.7.1.37)
(Leucine-zipper protein kinase) (ZPK) (Dual leucine zipper bearing Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus musculus (Mouse). kinase) (DLK). MAP3K12 OR ZPK. 

[1] SEQUENCE FROM N.A

NCBI\_TaxID=10090

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Phosphorylation;
DOMAIN 158
NP_BIND 164
BINDING 185
ACT_SITE 269
DOMAIN 56
DOMAIN 698
DOMAIN 753
MUTAGEN 185
CONFLICT 18
CONFLICT 382
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"Characterization of dual leucine zipper-bearing kinase, a mixed lineage kinase present in synaptic terminals whose phosphorylation state is regulated by membrane depolarization via calcineurin.";

J. B.O. Chem. 271:16888-16896(1996)
                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \frac{1}{1} \ \frac{1}{1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blouin R., Beaudoin J., Bergeron P., Nadea "Cell-specific expression of the ZPK gene DNA Cell Biol. 15:631-642(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ICR/Swiss Webster; TISSUE-Brain; MEDLINE-96365388; PubMed-8769565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ICR/Swiss Webster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-95074107; PubMed-7983011;
Holzman Lipy, Merritt S.E.; Fan G.;
"Identifygation, molecular cloning, and characterization of dual electine zipper bearing kinase. A novel serine/threonine protein kinase that defines a second subfamily of mixed lineage kinases.";
J. Biol. Chem. 269:30808-30817(1994).
                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; SMART; SM00221; STYKC;
                                                                                                                                                                                                                                                                        InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                HSSP; P06213; 11RI
MGD; MGI:1346881;
                                                                                                                                                                                                                                                                                                                                          EMBL; U14636;
EMBL; U23789;
                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION OF MAP3K12, AND MUTAGENESIS MEDLINE-96279269; PubMed-8663324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CD-1; TISSUE-Brain;
                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + a protein - COFACTOR: Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: Magnesium.
SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated
TISSUE SPECIFICITY: Expressed in brain, kidney, lung, hear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hiol. Chem. 271:16888-16896(1990).
FUNCTION: May be an activator of the JNK/SAPK pathway.
Phosphorylates beta-casein, histone 1 and myelin basic
                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE SER/THR MAP KINASE KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            testis, gastrointestinal tract, stomach, Within the nervous system, predominantly enriched in synaptic terminals.
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                                                                                                                                                                                                                                    PS00107;
                                                                                                                                                                                           Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                          AAB17123.1; -.
                                                                                                                                                                              Magnesium;
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172
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269
62
671
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382
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                                                                                                                                                                                 Membrane
                                                                                              BY SIMILARITY.
POLY-GLY.
POLY-PRO.
                              K->A: NO CATALYTIC ACTIVITY E->A: NO CHANGE.
V -> A (IN REF. 2).
                                                                    POLY-GLU.
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              Ser/Thr. Phosphorylated in cyto dephosphorylated when membrane-
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       brain, kidney, lustomach, liver and
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RESULT
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Best Local
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase kinase kinase
(MAPK-upstream kinase) (MUK)
                                                                                                                                                                                          This
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAT
                                                                                                                                                                                                                                                                                                      Oncogene 12:641-650(1996).
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FACTOR PUMEDLINE-96226099; Pumer Trawa M.,
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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Activation of the JNK pathway by di
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                                                                                                                                                                                                                    associated (By similarity).
SIMILARITY: BELONGS TO THE SER/THR
                                                                                                                                                                                                                                            similarity).
PTM: Autophosphorylated on
                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                     COFACTOR:
                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                           MAP KINASE KINASE KINASE SUBFAMILY
                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                   under basal conditions and
                                                                                                                                                                                                                                                                                              Phosphorylates beta-casein,
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8; Conserv
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517
794
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Pred. No.
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                                                                                                                                                                                                                                                                                               histone
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                                                                                                                                                                                                                                                             and membrane-associated
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                                                                                                                                                                                                                                                                                                       JNK/SAPK
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                                                                                                                                                                                                                                                                              phosphoprotein
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; Murinae; Rat
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                                                                                                                                                                           restrictions
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                                                                                                                                                                                                                                             cytoso]
                                                                                                                                                                                            a collaboration
                                                                                                                                                                                                                                                                                                protein
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NP\_BIND BINDING ACT\_SITE the European Bioinformatics Institute. The state of the property of the statement as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch). PROSITE; Pfam; PF00069; pkinase; SMART; SM00221; STYKC; 1 EMBL; D49785; HSSP; P06213; Phosphorylation; DOMAIN 158 InterPro; IPR000719; Euk\_pkinase. InterPro; IPR004040; STY\_pkinase. InterPro; IPR002290; Ser\_thr\_pkin Transferase; PROSITE; PS50011; PROTEIN\_KINASE\_DOM; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG. PS00108; PROTEIN\_KINASE\_ST; 1. 158 164 185 269 Serine/threonine-protein BAA08621.1; -. Hagnesium; Membrane.
399 PROTEIN K
172 ATP (BY S
185 ATP (BY S
269 BY SIMILA thr\_pkinase PROTEIN KINASE.
ATP (BY SIMILAR:
ATP (BY SIMILAR:
BY SIMILARITY. is not removed. (BY SIMILARITY). kinase; (See http://www.isb-sib.ch/announce/ as its content ATP-binding; and for ö

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Query Match
          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gozayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
A Adams tides P.G., Scherer S.E., Hichards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,
R. Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
R. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
R. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R. Berton S.C., Busam D.A., Buther H., Cadleu E., Center A., Chandra I.,
R. Burtis K.C., Busam D.A., Buther H., Cadleu E., Davies P.,
R. Cherry J.M., Cawley S., Dahlker C., Davenport L.B., Davies P.,
R. Cherry J.M., Cawley S., Dahlker C., Davenport L.B., Davies P.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
R. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
R. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
R. Harris N.L., Barvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
R. Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Luu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
R. Holson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacler F., Shen H.
R. Palazzolo M., Piltman G.S., Pan S., Pollard J., Rheese M.G.,
R. Palazzolo M., Piltman G.S., Pan S., Pollard J., Schol H. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blochlinger K., Bodmer R., Jack J., Jan L.Y., Jan Y.N.;
Prinary structure and expression of a product from cut, a locus
involved in specifying sensory organ identity in Drosophila.";
Nature 333:629-635(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spier E., Sprading A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remington K., Saunders R.D.C., Scheeler F., Shen H. Siden-Klamos I., Simpson M., Skupski M.P., Smith T., zradling A.C., Stapleton M., Strong R., Sun E.,
                                                                                                                                                                                                                         ö
                                                                                                                                                                       Score 44; DB 1; Length 888;
Pred. No. 46;
4; Mismatches 5; Indels
                                                                           POLY-GLU.
52AD964006BAE149 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    HWCU_DROME
P10180; Q9W3Q6;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
     POLY-GLY.
POLY-PRO.
POLY-PRO.
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MEDLINE-20196006; Pubmed-10731132;
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62 PC
671 PC
701 PC
758 PC
96307 MW;
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Best Local Similarity 47.1%;
Matches 8; Conservative
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751 SSEEEGANDSEVELPP 767
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                                                                                                  SEQUENCE. 1 888 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SUBCELLULAR LOCATION: Nuclear (Probable).
IISSUE SPECIFICITY: DEFECTED IN MANY CELLS IN THE CENTRAL NERVOUS SYSTEM, ALL EXTERNAL SENSORY ONGANS, SOME PERIPHERAL NUCRONS, AND IN THE NON-NEURAL CELLS OF THE SPIRACLES AND THE MALPIGHIAN
                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: CELL-SPECIFIC PATTERN OF EXPRESSION. BROADLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPRESSED DURING EMBRYONIC DEVELOPMENT.

DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY PARTICIPATE IN
REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: CONTAINS 3 CUT DOMAINS.
-i- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
CUT 1.
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ASP/GLU-RICH (ACIDIC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flybase; FBgn0004199; ct.
InterPro; IPR003350; CUT.
InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
Pfam; PF02776; CUT; 3.
Pfam; PF00046; homeobox; 1.
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PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
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HSSP; P04002; 1WFA.
TRANSFAC; T02004; -.
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Length 2175;

Score 44; DB 1;

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                                                                                                                  Pfam; PFU405; GatB; 1.
Pfam; PF02162; GatB,N; 1.
Pfam; PF02304; GatB,N; 1.
PR0SITE; PS01234; GATB; 1.
Protein biosynthesis; Ligase; C
                                                                                                                                                                                                                                                                                                                                                                           delth: functional analysis and comparative genomics.";

J. Bacteriol: 179:7135-7155(1997).

GLN-TRNA(GLN) IN ORGANISMS HIGH ETANSAMIDATION OF CORRECTLY CHARGED GLN-TRNA(GLN) THOOGH THE TRANSAMIDATION OF MISACTLATED GLU-TRNA(GLN) ATP THROUGH REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH AN ACTIVATED GAMMA-PHOSPHO-GLUTENAVI-TRNA(GLN) (BY SIMILARITY).

AN ACTIVATED GAMMA-PHOSPHO-GLUTAMAYL-TRNA(GLN) + L-GLUTAMINE - ADF + PHOSPHATE + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMATE.

1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE.

1- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).

1- SUBUNIT: BELONGS TO THE GATB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000
30-MAY-2000
16-OCT-2001
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GATH OR WHITE OF THE CONTROL OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Oil D.,
Spadaffora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels C. J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
Complete genome sequence of Methanobacterium Thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith D.R., Doucette-Stamm L.A., Deloughery C., Landredge T., Bashirzadeh R., Blakely D., Cook R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota;
Methanothermobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales;
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                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                            EMBL; AE000893; AAB85762.1; -.
InterPro; IPR003789; DUF186.
InterPro; IPR001773; Gln_amidotransf_B
                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                         Mismatches
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Gar
"Alignment of disulfide bonds of the extracellular domain
interferon gamma receptor and investigation of their role
biological activity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89003065; PubMed-2971451; Aquet M., Dembic Z., Merlin G.;
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zauodny P.J., Narula S.K.;
"Crystal structure of a complex between
soluble high-affinity receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93183911;
                                                                                                                                                                                                                                      *Observation of an unexpected third receptor molecule structure of human interferon-gamma receptor complex.*
Structure 8:927-936(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95342235; PubMed-7617032;
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                                                                                                                                                                                                                                                                                                             MEDLINE=20444407; Thiel D.J., le Du
                                                                                                                                                                                                                                                                                                                                                                               "Neutralizing epitopes on the extracellular interferon gamma receptor (IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis and X-ray crystal structure of the A6 fab-IFNgammaR1-108 complex."; J. Mol. Biol. 273:882-897(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sogabe S., Stu
Winkler F.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS)
                                                            SUBCELLULAR LOCATION: Type I membrane protein.
PTM: PHOSPHORYLATED AT SER/THR.RESIDUES.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN SIMILARITY: CONTAINS 2 FIBRONGETIN TYPE III-LIKE DOMAINS SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RISINILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RIDATABASE: NAME-PROW; NOTE-CD guide CDw119 entry; DATABASE: NAME-PROW; NOTE-CD guide CDw119 htm.
                                                                                                                                                                                         SUBUNIT: MONOMER
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SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
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|etazoa; Chordata; Craniata; Vertebrata;
|etazoa; Primates; Catarrhini; Hominidae;
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(Rel. 14, Last seq
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Gaps

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01-DEC-2001 (TIEMBLI'el. 19, Last annotation update)
TISSUE FACTOR PATHWAY INHIBITOR BETA (HYPOTHETICAL)
                                                                                                          PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 2.
Serine protease inhibitor; Hypothetical protein.
SEQUENCE 251 AA; 28652 MW; 9B3F276A52B4F0B9
                                                                                                                                                                                            InterPro; IPRO02223; Kunitz_BPTI
Pfam; PP00014; Kunitz_BPTI; 2.
PRINTS; PR00759; BASICPTASE
SMART; SM00131; KU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang J.-Y., Monroe Submitted (AUG-1997)
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Mammalia; Eutheria;
NCBI_TaxID-9606;
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        Score 96; DF
Pred. No. 8.1
0; Mismatches
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Catarrhini; Hominidae;
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        DB 4; I
8.1e-08;
hes 0;
                                              Length 251;
                                                                                                                 CRC64;
           Indels
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ue80 homo sapien
000145 homo sapien
000145 homo sapien
Q9wbt6 gb virus c
080931 human papi1
Q9igt8 porcine ade
Q9igt8 porcine ade
Q9if18 parabidopsis
062156 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9n0h2 balaenopter
Q99848 homo sapien
Q96a66 homo sapien
Q07527 bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91tl4 tupaia herp
Q9vxq6 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                093955 yarrowia li
09z8h4 chlamydia p
062511 mus musculu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9sz99 arabidopsis
O70618 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O66541 aquifex aeo
Q62509 mus musculu
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Result No.

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Gaps

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Yamada K., Printz R.L., Osawa H., Granner D.K.; "Human ZHX1: cloning, chromosomal location, and interaction with transcription factor NF-Y.";
                                                                                                                              Biochem. Biophys. Res. Commun. 261:614-621(1999)
                                                                                                                                                                                                                                                                                                                                                            SMART; SM00355; ZnE_C2H2; 2.
PROSITE; PS50071; HOMEOBOX_2; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                    TRANSFAC; T04355; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR000822; Znf-C2H2.
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InterPro; IPR000822; Znf-C2H2
                                                                                                                                                                                                                                                                                                                                            SMART; SM00389; HOX; 5.
SMART; SM00355; ZNE_C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 02, TrEMBLrel. 02, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.1%;
                                                                                                                                                                                                                                                                                                 Pfam; PF00046; homeobox; 4. Pfam; PF00096; zf-C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.18;
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Best Local Similarity 61.1
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLY DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                          SEQUENCE FROM N.A.
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01-FEB-1997
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                                                                                                                                                                                                                                                                                                                Sukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NOBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor.
SEQUENCE 2225 AA; 242198 MW; A5DDBAE9D2A7B02A CRC64;
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ZINC FINGER HOMEOBOX PROTEIN ZHXI (ZHXI PROTEIN).
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Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSO0280; BPTL_KUNITZ_1; 8.
PROSITE; PSS0279; BPTL_KUNITZ_2; 10.
PROSITE; PSO0484; THYROGLOBULIN_1; UNKNOWN_1
                                                                                                                                               2225 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterpro; IPR002899, EB.
nterpro; IPR00223; Kunitz_BPTI.
nterpro; IPR000716; Thyroglobulin_1.
fam; PF000014; Kunitz_BPTI; 10.
fam; PF00086; thyroglobulin_1; 1.
                                                                                                                                                                                           Created)
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MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Investigating biology.";
Science 282:2012-2018(1998).
EMBL: 292815; CAB07294.1; -.
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55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00759; BASICPTASE
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                   29 DSEEDERTIITOTELPP 46
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                                                                                                                                               PRELIMINARY;
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1 DSEEDEEHTIITDTELPP
                                                                                                                                                                                                                                                                                      Caenorhadditis elegans
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Best Local Similarity
Matches 10; Conserv
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Barthelemy I., Carramolino L., Gutierrez J., Barbero J.L., Marquez G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                                                              ö
                                                                                                Score 51; DB 4; Length 873;
Pred. No. 7.4;
1; Mismatches 6; Indels
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z$4200; CAA90905.1; -.
1; Homeobox; Nuclear protein; Zinc-finger.
873 AA; 98097 MW; 66CFICEC5EF824E5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and five homeodomains.";
Biochem. Biophys. Res. Commun. 224:870-876(1996)
                                                                                                                                                                                                                                                                                                                                                                                                             873 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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SMART; SM00355; ZnF_C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; zinc-finger
873 AA; 9762
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SEQUENCE FROM N.A. TISSUE-LIVER; CBI\_TaxID=9606;

Q9UKY1

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Best I
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Best Local Similarity
Matches 11; Conser
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01-JUL-1997
01-JUL-1997
01-DEC-2001
                                                                                       043863 PRELIMINARY; PRT; 677 AA.
043863;
01-JUN-1998 (TIEMBLEGL. 06, Created)
01-JUN-1998 (TIEMBLEGL. 06, Last sequence update)
01-DEC-2001 (TIEMBLEGL. 19, Last annotation update)
MEMBRANE ASSOCIATED GUANYLATE KINASE 1 (FRAGMENT).
MAGI-1.
                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
SEQUENCE FROM N.A.
MEDLINE=97369492; PubMed=9225980;
Margolis R.L., Abraham M.R., Gatchel
Breschel T.S., Stine O.C., Callahan
                                                        Homo sapiens (Human). Eukaryota; Metazoa; C Mammalia; Eutheria; P
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                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002349; WW_domain.
Pfam; PF00397; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 cloning of ligand targets."
J. Biol. Chem. 272:14611-14
EMBL; U96115; AAC51326.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of novel human WW domain-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-97313427; PubMed-9169421;
MCConnell S.J., Uveges A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                           SMART
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                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001202;
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                                                                                                                                                                                                  103
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                                                                                                                                                                                                           DSEEDEEHTITTOTELPP 18
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SM00456; WW; 1.
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                                                                                                                                                                                                                                                                                                                  PS50052;
PS01159;
PS50020;
                                                                                                                                                                                                                                                                                       224
224 AA;
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                                                                                                                                                                                                                                       Conservative
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WW_DOMAIN_1; 1.
WW_DOMAIN_2; 1.
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24816
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Primates;
                                                           Chordata;
Primates;
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61.1%;
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61.1%;
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19,
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Last annotation update)
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Pred. No. 2.1;
2; Mismatches
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Pred. No.
   Gatchell
allahan C.
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                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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   S.B., Li :
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   S.H., Kidwai A.S.,
s M.G., Ross C.A.;
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RESULT 075085

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Best Local Similarity 61...
Matches 11; Conservative
                                                                                                     Query Match
Best Local
                                                                                 Matches
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01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
NON_TER
SEQUENCE
                                                                                                                                                               protein.";
submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF401655; AAK94065.1; -
SEQUENCE 1160 AA; 126958 MW; 78FE5B621AC295B0 CRC64
                                                                                                                                                                                                                                                                                                                                                      MAGG-IA.
Homo sapiens (Human).
Homo sapiens (Human).
'`~rvota; Metazoa; Chordata;
'`~rvota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0403; WWDOMAIN.
SMART; SM00072; GuKC; 1.
SMART; SM00228; PDZ; 2.
SMART; SM00456; WW; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00595; PDZ; 2
Pfam; PF00397; WW; 2.
                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96QZ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000619; Guan InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U80754; AAC04844.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain-containing proteins Mol. Cell. Neurosci. 11:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood J.D., Yuan J., Margolis R.L., Colomer V.,
Kaminsky Z., Kleiderlein J.J., Sharp A.H., Ross
Kaminsky I., Kleiderlein J.J., Sharp A.H., Ross
Kaminsky Z., Kleider J., Sharp A.H., Ross
Kaminsky J., Kleider J., Colomer V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM, N.A. MEDLINE-98313405;
                                                                                                                                                                                                                                                                  "MAGI-1: a widely expressed,
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNAs with
254
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                     1 DSEEDEEHTIITDTELPP
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  DSGEQEEHT-LQETALPP
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                                                                                                   Similarity
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PS50106;
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677
677 AA;
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WW_DOMAIN_2;
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WW_DOMAIN_2; 2.
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677
74507 MW;
                                                                                                     52.6%;
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  270
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19,
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Last sequence update)
Last annotation update)
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Pred.
                                                                                                     Score 50.5;
Pred. No. 1
                                                                                                                                                                                                                                                                      alternatively spliced tight
                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                 Mismatches
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                                                                                                                        Length 1160;
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                                                                                    Indels
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PRELIMINARY;

EQUENCE FROM N.A.

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Laura R.P., Lasky L.A.;
"MAGI-1: a widely expressed, alternatively spliced tight junction
protein ":
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF401656; AAK94066.1; -
SEQUENCE 1462 AA; 161609 MW; 2E98A448A9E7DF89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. Submitted (NOV-2001); AAH17179.1; --
Hypothetical protein. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555A6529B6CEB211 CRC64;
                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
    4
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  Mismatches
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Pred. No. 15;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                       Created)
                                                                                                                                                                               PRT;
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TISSUE-EYE, AND RETINOBLASTOMA;
  5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%;
                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                  254 DSGEQEEHT-LQETALPP 270
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                           1 DSEEDEEHTIITDTELPP 18
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  Conservative
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                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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Best Local Simi
Matches 11;
  11;
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Q91LG7
ID Q91LG7
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  Matches
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Blochem. Blophys. Res. Commun. 247:597-604(1998).
EMBL; AB010894; BAA32002.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                  Homo saplens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Laura R.P., Lasky L.A.;
"MAGI-1: a widely expressed, alternatively spliced tight junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                initatsuch T., Futamura M., Oda K., Nishimori H., Nakamura Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01159; WW_DOMAIN_1; 2.
PROSITE; PS50020; WW_DOMAIN_2; 2.
SEQUENCE 1256 AA; 136981 WW; 83FADE2091A4C8E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 1287 AA: 140439 MW; C676655657BDE0D5 CRC64;
                                                            Last sequence update)
Last annotation update)
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Last annotation update)
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PRT; 1256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1287 AA.
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Pred. No. 13;
2; Mismatches
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Pred. No. 13;
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                                         Created)
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                                                                                                                                                                                                                                                        (EDLINE-98321173; PubMed-9647739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pro; IPR001202; WW.
Pro; IPR002349; WW_domain.
PF00625; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.6%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.6%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                   01-NOV-1998; (TremBirel. 08, 01-NOV-1998; (TremBirel. 08, 01-DEC-2001 (TremBirel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                BAI1-ASSOCIATED PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00403; WWDOMAIN.
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ROSITE; PS00856;

RINTS;

ROSITE;

PRELIMINARY;

620960

RESULT

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MAGI-1B ALPHA BETA

01-DEC-2001 01-DEC-2001

NCBI\_TaxID=9606;

protein.";

Query Match Best Local Similarity

Gaps

Gaps

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Best Local s
Matches 9
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Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-GSS1 / DSM 4299 / JCM 9571;

STRAIN-GSS1 / DSM 4299 / JCM 9571;

MEDLINE-20570466; PubMed-11121031;

Kawashima T., Amano N., Koike H., Makino Kawashima - Ohya Y., Watanabe K., Yamazaki Kawashima - Vamamoto Y., Aramaki H., Makino Yamamoto Y., Aramamoto Y., Ara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q978Q6
Q978Q6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF369029; AAK77742.1; SEQUENCE 1044 AA; 117929 MW; 9E4E3EC532320B3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=21342572; PubMed=11448154;

van Hulten M.C.W., Witteveldt J., Peters

Tarchini R., Fiers M., Sandbrink H., Lank

"The white spot syndrome virus DNA genome

Virology 286:7-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91LG7;
01-DEC-2001 (TrEMBLrel.
DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
ORF73 //
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoplasma volcanium. Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVG1406112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White spot syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9265
                                                                                                                                                                                                                                                                                          sequence of Thermoplasma volcanium. Proc. Natl. Acad. Sci. U.S.A. 97:14
                                                                                                                                                                                                                                                                                                                                                      Nunoshiba T., Yamamoto Y., Aramaki H., Makir
"Archaeal adaptation to higher temperatures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=50339;
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395
                                                                                                                                                                                                                                                                            nterPro;
                        DSEEDEEHTIITDTELPP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSEEEEEEDIIVDDE 166
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DNEEDYKRYLITDTGISP
                                                                                                                                                                                                               PF01558; POR; 1.
PF01855; POR_N; 1.
                                                                          Similarity 50.09; Conservative
                                                                                                                                                                                             proteome.
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IPR002880; POR_N.
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1 (TrEMBLrel. 19
OXIDOREDUCTASE.
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                                                                                                                                                                            ΑĄ,
                                                                                                                                                                            63978
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                                                                                           50.0%;
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                                                                                                                                                                            MW;
                                                                        Score 48; DB Pred. No. 15; 4; Mismatches
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Last annotation update)
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Last
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Pred.
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                                                                                                                                                                            DD061F862266DFCD CRC64;
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annotation
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ki M., Kar
Makino K.
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19;
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                                                                                                                  17;
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                                                                                                              Length 585;
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                                                                                                                                                                                                                                                                                                                                                                                                  Kawamoto
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RESULT ON MESSAGE STORY OF STO
RESULT
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Best Local S
Matches 9
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SMART; SMO0181; EGF; 11.

SMART; SM00179; EGF_CA; 9.

PROSITE; PS01177; ANAPHYLATOXIN_1;

PROSITE; PS01178; ANAPHYLATOXIN_2;

PROSITE; PS00110; ASX_HYDROXYL; 5.

PROSITE; PS01186; EGF_CA; 9.

Calcium_binding; EGF-like_domain;
                                                                                                                                                                                                                          OPY2 OR P9513.9 OR YPRO75C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaleeae; Saccharomycetaleeae; Saccharomycetaleeae; Saccharomycetaleeae; Saccharomycetale
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InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99K58;
01-JUN-2001
                  STRAIN-S288C (AB972);
Johnston M., Andrews S.
Favello A., Fulton L.,
Hallsworth K., Hawkins
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                               206810
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SEQUENCE 1174 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2001)
EMBL; BC005443; AAHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILAR TO FIBULIN 2.
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                     Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PF01821; 
; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEEEEEETLVTE---PP
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9; Conserv
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EGF; 6
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ANAPHYLATOXIN_2;
ASX_HYDROXYL; 5.
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Rodentia;
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126460 MW; 8
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EGF-like.
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                  Gattung S., Gre
J., Hillier L.,
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17,
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    Latreille
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Last annotation updat
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                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47.5;
Pred. No. 38
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                                                                                                                                                                                                                                                                           Saccharomycotina; Saccharomycetes;
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Sciurognathi; Muridae
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                                      Greco
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                                  Cooper J., Ding H., Du
eco T., Kirsten J., Kuca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                     Saccharomyces
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Langston

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Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Materston R.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Edgeois N., Horecka J., DePinho R.A., Sprague G.F., Tyers M., Elledge S.J.; Genetics 0,040(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 3; Length 360;
Pred. No. 13;
4; Mismatches 5; Indels
                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
Waterston R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                      73; AAG68126.1; -.
[6263; AAB81506.1; -.
5279; OPY2.
360 AA; 38901 MW; 6D444AFA25042FFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.18;
Matches 8; Conservative
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Search completed: September 20, 2002, 10:31:03 Job time: 225 sec

1 DSEEDEEHTIITOTELP 17 | ::|||:|| | :|| | :|| | 334

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